

## FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC  
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG  
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG  
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC  
TCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC  
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG  
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC  
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAAATGAAA  
CGTGAAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT  
TACAAAT

## **FIGURE 2**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCVPKGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

09978192-101501  
TOSTOT-26182660

### FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCCACGGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCCTGATC  
CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA  
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGT  
GTGAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC  
TGCCGTCTTTTACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC  
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCTTT  
CCTTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTTCTCTTAAACACAAATACAGTTT  
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC  
TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC  
GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC  
TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC  
AAGAAGTTACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGACAGAAC  
TCTGTGTTGTTCTTTTGCAGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTGCG  
GATCATCGTCCTCATCGCCAGCCTCGTGGTCTACCTACCTGGGGGTGCACGGTGCAGCCC  
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA  
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG  
AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTTTTGTTTTGGTAAT  
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT  
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC  
TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC  
TCCTCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
CACCTGTCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG  
TTAAAACTCGGCTTCCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG  
GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTTCACTGAGGAACGGAGACCTGTGAC  
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG  
GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA  
GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCAAAAA  
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC  
CTTTCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTATGTTTT  
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTGCTGTAGGGTAAC  
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAATGTACTACGGTACTTCCCTCCACACCATACGATAAAGCAAGACATTTTATAACG  
ATACCAGAGTCACTATGTGGTCTCCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA  
TATTTTTCTAAGTTTTGGAAAGCAGGTTTTTTTCTTTAAAAAAATTTATAGACACGGTTCCT  
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCCTAAACAAAAAAATATTTTAAAGATA  
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCGC  
ATTTTCAATAAAATGTCTCTAATAACAAAAA

## **FIGURE 4**

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSDFKNVGLVVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIINKLHHVDES  
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPLLIPILSLYMGALVRCTTLCCLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQIRISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNPNPSN  
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVPLR  
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVBGATLGVGSL  
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEEVTDIVEMRENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

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"FOSTOT" 26782660



## **FIGURE 5**

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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## **FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCTTTGCGGATTTTCT  
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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## FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA  
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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TOSTOT 26182660

## FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGAGAGTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCCTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCCTACTTCGGCGTCGTGGGCTCCTTCTTCTTCA  
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACTGAGCCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCTGCCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCTCCTGTGCACCCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCTTCCCCTCCTCCCTGT  
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACCTCCACACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT  
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTGGAATTCTGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

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## **FIGURE 9**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFFLGVLVSIIMLSPGVE  
SOLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLILIQLVLLIDFAHSW  
NQRWLKAAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC  
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVTSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

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## FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG  
TGA CTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATAACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA  
GCTGTCACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTACAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA  
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTTCTTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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## **FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDVQSAH  
RAATRGFIIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 76-96 and 171-195

#### **N-glycosylation site:**

amino acids 153-156

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TOSTOT.26182660

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG  
GCTGGCGCCGAACC

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"05101" 2618/660



## FIGURE 13

TCAAGTTTGTCCGTAGGTCTGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

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TOSTOT"26T8/660

## FIGURE 14

GAGCCGCCGCCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCGGCCCGCCCCACCCACGTCT  
GCGTTGCTGCCCCGCCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT  
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGG  
GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT  
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCTTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAAACATCATCAGGTGTTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTTATT  
GTTCAAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTTAACCCTAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG  
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA  
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCATTCTTTGATGAGAAAACAAGGAAGAT  
TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTTCTGTTAAGCTCCATTTGCCAGT  
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGAATTATATATTTTTACT  
CTATGTTTCTCTACATGTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCACTGTCGGGCACTGTCCACTGTGGCCTT  
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC  
TGAAAAAGAGTGGAATTTTATTAATAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATTCCCAATTTTTTTTTGGTCTTTTATAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA  
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT  
GTCTTAGGAAATTGTGGTTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA  
AAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG  
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT  
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG  
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTGA  
ATTAAAAGAAAGTAATGGAAG

09578192 : 101504

## **FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWL  
TYRYRNQKDPRANPSAFL

### **Signal Peptide:**

amino acids 1-34

### **Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

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105101-26182660

## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCTAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

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## FIGURE 17

AATCCCAAATTCCCAATTTTTTTGGNCTTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

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## FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

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## FIGURE 19

CAGTCACCAATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCTTGGTGTG  
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAACTGTTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCCG  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGA  
GGAGGCCCTGGGCCTCTGCCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
CAGGATGTGAGAGTCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTCCTGTCCTGCACATATGCATAAGTA  
CTTTTACAAGTTGTCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
GGCAGTACCCCAACAACGAAAAATAATCTGGCCCAAATGTGAGTTGTAAGTGTGAGTTTGAAGAA  
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATAACAGTCTTTAGCTGGTGTCTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG  
ACTCTGTCGTTGCCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG  
TTGTTTGTAGCCTAA

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## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQCQAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSAAPTLPNPAPQKSAAPGTAPPEEAPGPLPPPPTPSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

### **Signal sequence:**

amino acids 1-17

### **Leucine zipper pattern sequence:**

amino acids 12-33

### **Protein kinase C phosphorylation site:**

amino acids 353-355

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105101 26184660



## FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGG  
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCAGGAGATGTATCCCTCCAATTGAGCACCTTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCTTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCCAGATCAATGGCAACTACGCCCCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTAAAAAATGCCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCCCTGGATAGCCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRHLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDDMDGYLGGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

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FOSTOT 26T82660

[illegible]

GCGCCGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGGCCCGGCACAT  
GGCTGCGAGGACCTCGCGGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCGGTCGGA  
GGCGCCCGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
GGGATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTTCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTGCGAGGAGATGCCTCCTTGCGAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTTCAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCATTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
GACTACAAACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA  
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCACACCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA  
ACGGTCTTGAATTACAATGGACTTGACTCCACGCTTTTCTAGGAGTCAGGGTCTTTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
TGTGAGCATTGCACGGAACAGATTTCAGATGAGCATTTTTCTTATACAATACCAAACAAGCAA  
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAATT  
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTCTATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTTCAAAT  
CAGATGCCTCTAAGGACTTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT  
TATCAACGTCCTTAGAAAGAAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAAATGTGAAACCAGAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

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## FIGURE 25

GTCTGTTCTTTGCTCTCTCGCGCCAGTCTCTCTCCCTGGTTCTCTCTCAGCCGCTGTCTGGAGGAGAGCACC CGGA  
GACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCCCTAG  
AGCCTCCCTTGGCGCCTCCCTCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCCG  
GCCCCGGAGGCGGGCGGTGGATGCGGGCGCTGGGCAGAAAGCAGCCGCGGATTCCAGCTGCCCCGCGCGCCCCGGGCG  
CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACC CGCCTCGCCTCTGCGAGCCGCATC  
GCCCCGCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCTCTGCTTGGATTCTTTAGCACCACCACAGCTCAG  
CCAGAACAGAAAGGCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCGAGCAGTTGCCCT  
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCCATGGCCCAATG  
ATTGAGAAATTACCTTGTGCTGCCCTTGACTGACCGAGAATGCACCTTGCCCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCATAACGGTGTGTCTGTGGGTGTGGGTGTGCGGAAGAAAGGGAAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT  
CTGAGTCAGAACCTGGTGGTGTGATCAAGCCGGGGACCAAGGAGACAGACAACGCTGTGTGGCACACTCCCGTCTTTC  
TCCAGCTCCACCTCACCTTCCCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT  
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTTCTGCTCTGTGTAGACCAAAGGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC  
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCTGAAGCTGCTGCCGTCCATGGAG  
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCTAGACAGAACCTACACAAG  
CATTTTGACATCAATGAGCATTGTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGTGTGTGGTGTGTTGGT  
TGCAGTATCCGGAAGGCTCGAGGACTCTGAAAAGGGGGCCCCGGCAGGATCCCAGTGCCATTGTGGAAAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG  
AGGAGGTTGTGCTTTTCTCAATGGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCGACTGGACC  
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG  
AAGATTTCGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG  
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA  
CAGGACAAGAACAAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC  
TCCGCTGAGCAGGAAGACGGTTCCTTTATTACCAAAGAAAGAAAGGACACAGTGTGTGCGGAGGTACGCCTGGAC  
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG  
ATTCCCAGGCTGAGGACAAACTAGACCGGCTATTGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
CTCTGACTCTGTTTATAGCCATCTTCCTGACCTGCTGTAGAACATAGGGATACTGCATTTCTGGAAATTACTCA  
ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTGTGTTGGGGTGTGTGTGTGTGTGT  
GT  
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAACCTGTTGTGAA  
ATACCCACCACTAAAGTTTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTATGTATTTTCAAGATTATTCTG  
TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTCAACCTACTTTTT  
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA  
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTATATTATG  
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC  
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTTAAGTGGCTT  
GACAACTGGGCCACCAAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT  
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAAATTTGCCAGCTTTGCTTTTAAAGATGTCTTG  
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGTTGGGATTTCCTTCACCAATT  
ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTTGTGG  
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAACATTAGGTGTTTGTTA  
AAAAA

09978192.101501

## FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQQPHHRHIL  
KLLPSMEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRRNGSFITKEKKDVTLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEEIGVKSQEASQTLSDSVYSHLPDLL

### Signal sequence:

amino acids 1-41

### Transmembrane domain:

amino acids 350-370

0978192-101501

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA  
 CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
 CATGGGGGAAAATGATCCGCTGCTGTTGAAGCCCCCTTCTCATTCGGATCGCTTTTTTGGCC  
 TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
 TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
 ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
 TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
 GAGTACCGCTGTGTCCGGGTGGGTGGT CAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
 GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC  
 TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTC  
 CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
 CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT  
 GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
 TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTATCAC  
 GCCCCGTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
 CCATCCAGGTGGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACCTGGTGGAGAAG  
 ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
 GGCCGGGGCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
 ACTTCCCCGATGGAAAAGTGTGCTGGACGT CAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
 GCCTCCCCTGTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
 GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
 TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
 TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
 CCGTGTACCTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA  
 GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
 GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCA  
 GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT  
 GTTTTTTGTTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA  
 TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCA  
 GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTTGTATTTTTTAGTAGAGAC  
 AGGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
 CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC  
 TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
 CTGGTTTTTCTCTCCAGGGTCTTGCAAAATTCTGACGAGATAAGCAGTTATGTGACCTCACG  
 TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCAGCCAGAAGTGCAGAACTGCAGTC  
 ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAACCCACCCTTTCTACTTCCAAGACTTAT  
 TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTTCATGATTTCTT  
 TGTAGCATTGTTGCTTGACGTATTATTGTCCTTTGATTCCAATAATATGTTTCCCTCCCT  
 CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAAATCATCCACTGAAA

09978192 101501

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKV TALHH  
SVYVREGCASGHVVT LQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWII TAAHCVYDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHA AVPLISNKICNHR  
DVG GGIISPSMLCAGYLTGGVDSCQGD SGGPLVCQERRLWKLVGATSFGIGCAEVNKP G VYT  
RVTSFLDWIHEQMERDLKT

### **Signal Peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 240-284

09978492 104504  
T05T0T 26T82660



## FIGURE 29

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT  
GCCAGAACGGCGCGCGCGCGCACGCACGCGGAGGAACTTTTTTAAAAATGAAAGGCTAGAAGA  
GCTCAGCGGCGCGCGCGCGCGCGCGAGGCTCCGGAGTGAATCGCCGAGGCAGGAAATCCCTCCGGTCCGCGA  
CGCCCGGCCCCGGCTCGGCGCCCCGCGTGGGATGGTGCAGCGCTCGCCCGCGGGCCCCGAGAGCTGCTGCACTGAAG  
GCCGGCGACGATGGCAGCGCGCCGCTGCCCGTGTCCCCCGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGTCT  
GCTCGCGCCCTGCGAGGCCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT  
TCGGAGTGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCGACT  
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAGAAATGAAGGTCTCATTGCCAGCAGTTTACGGAAAC  
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
ACGGGGATATTTCTGATTCAGCAGTCACTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA  
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCAGCGAAGAAGCTGAAAAGCGT  
CCGGGGATCATGTGGATCACATCACAAACACCAAACTCGCTGCAAGAATGTGTTTCCACCACCCTCTCAGAC  
ATGGGCAAGAAGGCATAAAAGAGAGACCTCAAGGCAACTAAGTATGTGAGCTGGTGATCGTGGCAGACAACCG  
AGAGTTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAAGAGATTTGCTAATCACGTTGACAA  
GTTTTACAGACCACTGAACATTGGATCGTGTGGTAGGCGTGGAGTGTGGAATGACATGGACAAATCTCTGT  
AAGTCAGGACCAATTCACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA  
TGACAATGCGCAGCTTGTGAGTGGGTTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG  
CACGGCAGACCACTCTGGGGGAATTGTGATGGACCATTCAGACAATCCCTTGGTGCAGCCGTGACCCCTGGCACA  
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
AGGAGGCTGCATCATGAACGCTTCCACCAGGTTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACT  
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTAACCTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCA  
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTGAATCGCTG  
CTGCAATGCCACCACCTGTACCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
GAAGCCTGCAGGAACAGCGTGCAGGGAATCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC  
TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT  
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA  
GAGAGTCAATTTCTGAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCCTTTGCCAAATGCGAGAT  
GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC  
CATAGAAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTTGGGCGATGA  
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA  
AAATATTAGTGTCTTTGGGGTTTACAGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACACAGGAAGAA  
CTGCCACTGCGAGGCCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCC  
CATCCGGCAAGCAGAAGCAAGGCAGGAAGTGCAGAGTCCAACAGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG  
ATCGCAGGAGCATGCGTCTACTGCCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCACTG  
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT  
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA  
CAGTGCAGGAAGGGCAGCGACTTCTGTTGAGCTTCTGCTAAAAATGACATGCTTCAGTGTGCTCCTGAG  
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC  
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGTTGGGCCCAGTGTCCCTTTCCCCAGTGACACCTCAGCCT  
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATATATGAAAAT  
AGCAGGGTTTTAGTTTTTAAATTTATCAGAGACCCTGCCACCCATTCCATCTCCATCCAAGCAAACTGAATGGCAA  
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC  
AGTACTCAGGTTTGGAGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCCTTCAATTAACAAGTAAGAA  
TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT  
GAAAT

09978192-101501

## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGLWIPVKSFDK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK  
YRPLNIRIVLVGVEVWVNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVGICYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLOQGGRIICRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGGQEPVGSQEHASTASLTLL

**Signal peptide:**

amino acids 1-28

09978192.101501

## FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANNTTCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

09978192.101501  
TOSTOT 25T82660

## FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCGCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT  
GAAACCATAACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA  
CTTTTAACAAAAAATTTGCATCACTTTTAAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGCAAATCTGCCT  
TTTTATAGATTTGTAAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCTACTTGCTATCTCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTGT  
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGAGTGGCT  
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL  
LHLYH

**Signal peptide:**

amino acids 15-27

09978192.101501  
TOSTOT" 26T8/660

[illegible]

CCGCGCGCGAGAGCGCGCCAGCCCGCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGG  
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCCGGGCCAGG  
AGGCGGCGCGCGCGCGCGCGACGGGCCCCCGCGGCGAGACGGCGAGGACGGACAGGACCCCGCACAGCAAGCACC  
TGTAACAGGCCGACATGTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTCATGTTCTTCGCGCCCTGGTGTG  
GACACTGCCAGCGGCTGCAGCCGACTTGGAACTGGGAGACAATAACAGCATGGAGATGCCAAAGTCT  
ATGTGGCTTAAAGTGGACTGCACGGCCCCACTCCGACGTGTGCTCCGCCCCAGGGGGTGCAGGATACCCACCTTAA  
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGCTCCTCGGGACTTCAGACACTGGAAACTGGATGC  
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGCCCCCGAGCTCAAGCAAG  
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC  
CGTGGTGTGGTCAAGTGCAAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCTTGAACATTCCGAACCTG  
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCTCGGAAACAGGTTCTGGCTATCCCACTC  
TTCCTGTGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAGCGGGATTGGAGTCACTGAGGGAGTACG  
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG  
CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA  
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA  
AAAAGGAATTCCTGGTCTGGCGGGGTCAAGATCGCCGAGTAGACTGCACCTGTAACGGAAATATCTGCAGCA  
AGTATTCCGTACGAGGCTACCCCACTTATGCTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA  
GAGACCTTGACTCGTTACACCGCTTTGTCTCTGAGCCAAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTCA  
CTCTCCTGCCAGCTCCCGCACCTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT  
GTTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTTCCAAGCCAACACACTCTACAG  
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGTCAGTGTGTGTAACATTTTCACTGGCGATA  
TATCCCCCTTGACCTTCTCTTGTAGAAATTTACATGGTTCTCTTTGAGACTAAATAGCGTTGAGGAAATGAAA  
TTGCTGGACTAATTTGTGGCTCCTGAGTTGAGTGATTTTGTGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC  
CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTACAGTTGACTCAATAC  
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC  
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC  
GTGCTGAGTAAGAGAAATGCTGATGCCATAAATTTATGTCGATAGTCTGTCAAATCAGTTACTGTTTCAAGGGAT  
CCTTCTGTTTTCTACGGGGTGAACACTGTCTTTAGTTCTCATGTTAAACAGGAAGCCAGGCCACATGAGCTGT  
TGGATGCTTTCTTCTAGAAAGGTAGGCATGGAAATTCACGAGGCTCATTTCTCAGTATCTCATTAACCTATTGA  
AAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTCCAGGCCCTGGGTATCCAGGGAGGC  
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAAAGG  
CTTGCTATACTTGGTCTGCTTCAAGGAGGTGCACCTTCTAATGTATGAAGAAATGGGATGCATTTGATCTAAGAC  
CAAGACAGATGTCACTGGGCTGCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGCTCCTCTA  
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA  
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCT  
CCCATAACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACCTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA  
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCCTTAAAGGAAATCTTTATTAATCACG  
TATGGTTCAAGATAAATCTTTTTTAAAAAACCCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA  
CACAACTTCAGCTTTGTCATCAGAGTCTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTCACACTAT  
GATACTTTCTAAATAAACTCTTTTTTTTTTAA

## FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH  
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLNWMQLQTLNEEPVTPEPEVEPPSAPE  
LKQGLYELSA SNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIK FYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

09978192-101501

## FIGURE 36

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGTTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTTCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA



## FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHHTISPGPKGDDGEKGDPEEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY  
RKFBVGQLDISIARLKTSMKFVKNIAGIRETEEFYIVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

**Signal peptide:**

amino acids 1-25

09978192.101501  
TOSTOT"26T82660

## FIGURE 38

GGTTCTATCGATTTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGCACTTTCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG  
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCCGCGC  
ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGCGCGGCGACAG  
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG  
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG  
GTTTCGGGCTGGCCAAGGCCGCGCTGCGCACTGCCTTTGTGCCACCCGCCCTGCGCCGGGGCC  
CCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG  
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGATG  
GGCCAGTGCCAGGATACTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
ACCTCTGGCACCACGGGCCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC  
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACTTGTCAACCAGCCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACTGGGAGCGT  
TTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGCTTTTACAAGC  
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTCCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGTAAGCCA  
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCC  
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG  
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL  
LLLKLHLWPQLRWLPADLAFVAVRALCCKRALRARALAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFFSYSEAERESNRAARAFLRALGWDWGPDGSDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGVPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQ GK  
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

### **Type II transmembrane domain:**

amino acids 45-65

### **Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

### **CUB domain protein motif**

amino acids 254-261

### **putative AMP-binding domain signature**

amino acids 332-343

### **N-glycosylation sites**

amino acids 37-40 and 483-486

09978192-101501

# FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
 CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATAACACTCGCTCTC  
 GCTTGTCCATCTCCCTCCCGGGGAGCCGGCGCGCTCCACCTTTGCCGCACACTCCGGC  
 GAGCCGAGCCCCGAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC  
 CCATGGTGGTTTTTTAAACACTTCTTTTCCTTCTCTTCTCGTTTTGATTGCACCGTTTTCCA  
 TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT  
 CCATCTGGCTTATAAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG  
 CTGGCAGAAGGGGGTGACGCTGGGCAGCGCGCAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT  
 CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTTGGGGTTTACCGAGCTGGATTTGTATG  
 TTGCACCATGCTTCTTGGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC  
 TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC  
 AAGGGATTGAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
 TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC  
 TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG  
 CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
 TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
 TCACAGAGCTGAAAAGGTACTACACTGGGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC  
 TTTTGGGCTCGGCTCCTGGAACGGATGTTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA  
 AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
 GGAAACTGAAGATTGAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
 ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGTGTATCCG  
 TGCCCTCATGAAGATGCTGTACTGCCATACTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA  
 ACACTACTGTCTCAACGTGATGAAGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
 TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
 TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
 ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC  
 CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA  
 GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
 AATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGC  
 GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
 GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
 TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
 CTAACAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
 CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTTTGTACCA  
 CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC  
 CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATA  
 ATCTTGGGTTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT  
 TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG  
 CAGTAATGCAATCTGCCTCCCTTTTTGTTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG  
 CTTCTCTTTCTTTCAGCTATCTGTGGGGACCTTGTATTCTAGAGAGAATTCTTACTCAA  
 ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
 CTCACGTTGTGAGGGTTTTTTTTTTCTCATTTAAAT

105101-25182650

## FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKS LNDMF  
VRTYGMLYMQNSEVFQDLFTTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNL FIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVS AKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

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## FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGGAAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCCTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGGGCGCTCTGGCCACGA  
AAAGTTCCTGTCCACTGTGATTCTCAATTCTTGTCTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTCTTGGTGGAAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAGAAAGTGAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG  
AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCACCTCCCAGCCCCATCTCA  
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAACACCTACTCTTG  
ACAAGCTCGCTGCCGAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT  
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACCTGTTTAC  
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAAATGGCACT  
TGGGTTTTTAACAGAAAAGAAATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG  
GGGATTACTATACACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA  
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTATTACCACTGCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC  
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTTCAACAACCTGGGACCGAACC  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC  
TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCAGAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAAGCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAGCAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACCTGTCTGCTCAGTG  
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG  
GTGAGTCCTGAGTTCCACTGCTGTGCTTCACTCAACTGACCAAAACACTGCTTTGAATTATAGGAGGAGAAACAATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

## FIGURE 42B

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTTGTATGTCTGTCATATGA  
CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTTCT  
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC  
ACAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTTCTAGTATAAAAAACCTAATTTATTTTTACA  
GAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTTATTTTTATTTTCTGCATACCATTAGAAGA  
ATTTTATTTTCATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTGAGACTA  
TAAAAACATCATTGAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
ATTACTTGGAATTCATGTTTGTGTCAGAGTTGAGACAACCTTATGTTTCTATCATAAACTATTTATGTATCTT  
AATTATTAATAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAAT  
GTATCATTGGTCTTAAAAATAAAAAATCTTTACTAATAGGCAATGGAAGGAATGGTTTGCTAACAACACAGTAA  
TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATATAATAACTAA  
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTTAAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAACCCC  
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC  
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT  
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC  
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT  
CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAAATTTTAAACATTTTATTTCTAGAAATATAT  
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG  
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA  
AAA

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## **FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLA AEGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC  
MPTRRGFDFTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA  
LKTYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWTYLTGIQES

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-37

#### **Sulfatases signature 1.**

amino acids 120-132

#### **Sulfatases signature 2.**

amino acids 168-177

#### **Tyrosine kinase phosphorylation site.**

amino acids 163-169

#### **N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

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## FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATGCCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCTGGGTGGCAG  
GTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTAGCATCGGCACGTCAGCCT  
GGGGTCTGTCACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT  
GCAGATGCTTTCCAGGATACACCGGGAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAA  
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA  
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTGGAAGCTACTACTGCAAATGTCACA  
TTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCAAAAATTAATAATGTTACCCAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACTTGCAGCCCTTCACTATGAAGAGATAGTTTCCAGAGGCGGGAACCT  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTACAAGAAAGACATTGGCCGATTGAAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAATTGAGTTGTATCAAGGAACTGATGC  
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGTATATTGCATCATAG  
GACCTCTGGCATTTTAGAAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA  
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGA  
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAATCTTTGTAATAATAA

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## **FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE  
ATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

### **Signal peptide:**

amino acids 1-21

### **EGF-like domain cysteine pattern signature.**

amino acids 80-91

### **Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

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TOSTOT-26781660

## FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGACAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGCTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGCTGTGCTCAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT  
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC  
ATGGATAACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC  
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

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## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLEGNLKEKDILVLPLDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRS LCMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPWAWWITNKMGGKKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

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## FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCTCACTGCTGCCCCTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
CAGTGGTCTTGGGTTCTCTGCAGCGTGAAGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGTGTATCTACAACCAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTGAGGAGATTCCGGGGGCCCCCTGTGCTGTGCCTCGAGCCTGACGGA  
CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT  
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGACAGGACACCCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG  
CTGCCCCTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCCTGAGGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTTGGGACGG  
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCAAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG  
CATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAAATGGCATTACTGCCCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT  
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTTAAACTTAAATAAATTGTTAC  
AAAATAAAA

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV  
PGEWPWQASVRROGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRLRLRLISRPTCNCIYNQLHQRHLSNPARGMLCGGPQPGVQGPCQGDSSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPDGERG  
WVLGRARPGAGISSLQTVPVTLTGPRACSRLLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEF  
GSCLANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

09978192-101501  
TOSTOT-26182660

## FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG  
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTTCGGCGGGGCAGCCCTGGCATGGGTGT  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACCAAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG  
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCAGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCAACCAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC  
CCCTCCTTCCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCACCATGGTGTATTCTGGGGCTGGGGCAGTCTTTTCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGEKSKTALQPLKHSDSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

09978192.101501  
"2618/660"



## FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCTCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAAGCTCATCATTCCTCCTGC  
TCTGGGCTATGGAAGAAGGAAAAGGTAAAATCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTCACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATAACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCCTGGTTCCTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTCTA  
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

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TOSTOT-26T82660

## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMVCVEKRKLIIPPALGYGKEGKGIIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDEDKDGFISAREFTYKHDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 176-179

#### **Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

#### **Endoplasmic reticulum targeting sequence.**

amino acids 208-211

#### **FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

#### **EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

#### **S-100/ICaBP type calcium binding domain**

amino acids 183-203

09978192 101501  
TOSTIT 2678660

## FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
CTGCCACCCCTCAACGTCCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCCCTCCAGTTCGCGATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTTGGTGTGATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGGCCACCTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCACATGTGAGGGTCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGCTGTACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTTGA  
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCACCCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT  
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGTGGATTACCTCCAT  
CTGTTTGTAGTAAATGGGCAAAACCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
GGAAGCAGAGGTTGCAGTGAAGTGAAGTAGTGTAGTGCCACTGCAATTCAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAA

09976192.101504

## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

09578192-101501  
TOSTOT-2518/660

## FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG  
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCC

09978192 . 101501

## **FIGURE 57**

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

09978192 101501  
105101 26182660

## FIGURE 58

TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT  
TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGACGTCACCCCCAGTGGTGTGCTGGTCC  
CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA  
CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAACCTGCTGCTGCCTGTCAATCATTGACTGCTGGATTGACAATA  
TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG  
GGAAGACCTTCTCACTGGAGTTCTTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA  
GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG  
AAAACGGGCCCTACTTCTTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC  
TGTTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCTGGAAGGACAAGT  
ATATCCGGGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCTTGGCTTCAGGAG  
ACAACAACCGGATCCCAGTCACTCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACCAGCTGGC  
TGCTGCCCTACAACACACATGGTCACTGAGAAGGTGTTCTGTCAGACACCCACAATCAACTACACACTGCGGG  
ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT  
ATGAGAGCTTCCCTGACCGTGACCCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGAAGAGTGCCC  
TGCAGTGGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTGTGCTCCTTGGGGCCCTGACTCCTGTGCCACAGGA  
CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTATGGCCACGCGTTTTTGCAAAGTTTGTGA  
CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGCTGTTTGTATCCTTTCTCT  
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGGA  
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCCCTGGTCCCAGTCCCTGGCTGGGGCCATG  
TGTCCCCCTATTCTGTGGGCTTTTCATACTTGCCCTACTGGGCCCTGGCCCCGAGCCTTCCATGAGGGATGTT  
ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCTTCCACACACCA  
GCCACAGATAGGCCTGCCACTGGTCACTGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCCCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGCGTTCTTCTGTTGGTCCCAGGC  
CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG  
CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTACCCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGA  
GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA  
CACTGCCACCCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC  
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC  
TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT  
CAGGGCTGCCTTCACTGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT  
GGGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCACTGGATTTTCTCTG  
TTGCATACATGCCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

09978192.101501

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPFGFKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVQVQTPPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Potential lipid substrate binding site:**

amino acids 147-164

#### **N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

#### **Lipases, serine proteins**

amino acids 189-201

#### **Beta-transducin family Trp-Asp repeat**

amino acids 353-365

FOSTOT" 26T8/660



## FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAC TGCCA  
GCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTTAGCTAGTGTTTTTTCCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG  
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGTAATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

09978192 101501

## **FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPOVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVLIGDLLFSALWTFLWFVGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

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105101 25784660

# FIGURE 62

GAGCCACCTACCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
 CCCGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
 ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGTACCTCCGCTGGTGCCCTGTTTGTGCTGCTG  
 GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGCGGAGGTGATGGTCAGC  
 CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCCAGGATCTTACCCGCCGGAATCTAGTGCC  
 TTCCGCACTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACCTTACTAC  
 AACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTCATTCTCCAAATCCCCGAG  
 CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACCTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC  
 TCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA  
 GACATAGCTGCATTGAATTCACGCTGGGTGTTGTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG  
 AAGGGCCCTGACCACCTGGCCCTCCAGCTGCCTGTGSCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG  
 CTGGAGTGGACGCTGGCAGAGTGGCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC  
 ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGT  
 GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCAGGCCTGT  
 GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC  
 TCGCCCCAAACCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGTTTGTATGCC  
 TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT  
 GGCTTGGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC  
 TCCAGATCTCCCTCACCGGGCCCCGGTGTGCGGGTGCACCTATGGCTTGTACAACAGTCGGACCCCTGCCCTGGA  
 GAGTTCTCTGTTCTGTGAATGGAATCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT  
 GAGAGAACTGCGTTTGCAGAGCCACATTCAGTGCAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT  
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCC  
 TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGCACTGTGATGGGCGGGCCGACTGCAGGGACGGC  
 TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTTGTTGGTGGAGCTGTGTCTCCGAG  
 GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC  
 TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGTGTGGACCGTGTCTCTGGGC  
 AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACAC  
 GAAGAGGACAGCCATGACTACGAGCTGGCGCTGCTGCAGCTCGACCAACCCGTGGTGGCTCGGCCCGCGTGGC  
 CCCGTCTGCCTGCCCCGCGCTCCCACTTCTTTCAGAGCCCGGCCTGCACCTGCTGGATTACGGGCTGGGGCGCCTTG  
 CGCGAGGGCGGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG  
 GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGT  
 GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCTTGGCGGGCTGGTTCAGCTGGGGCCTG  
 GGCTGTGGCCGGCCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG  
 ACCTGAAGAACTGCCCCCTGCAAAGCAGGGCCCACTCCTGGACTCAGAGAGCCAGGGCAACTGCCAAGCAGG  
 GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC  
 CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACC  
 CAGGCCCCACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCCTTCTTCCACTGCTGCCTAATGCAAG  
 GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG  
 CTGTTTGGGCAGCCTTGCCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT  
 GGAAGGTGCTCCCATCGGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGTGCCACTGTAAGCCAA  
 AAGGTGGGGAAGTCTGACTCCAGGGTCTTGGCCCCACCCCTGCCTGCCACCTGGGCCCTCACAGCCCAGACCCCT  
 CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 63**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLASSCLWHLQGPDLML  
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFSPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDICRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAACHCFQEDSMASVT  
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCEAYRYQVTPRMLCAGYRKG  
KKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 46-67

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

#### **N-glycosylation sites.**

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### **Kringle domains.**

amino acids 746-758 and 592-609

#### **Homologous region to Kallikrein Light Chain:**

amino acids 568-779

#### **Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

## **FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACCTATGGCTTGTACAACCAGTCGGACCCCTGCC  
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC  
CGTCTGCCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGA CT CAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

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## FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAACACCAAGAGGTGGTTTTTGTTTTTTAAA  
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGCGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTCAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGATGTCCTCCACACCTACACGCGTTCCCTTCGGCTTGAGCATTGGTATTAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCCT  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

09978152.101501

## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL  
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT  
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Lipases, serine active site.**

amino acids 163-172

#### **N-glycosylation sites.**

amino acids 80-83 and 136-139

09978192.101501

# FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC  
TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT  
CGGCAAAGTTTGGCCCCAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG  
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG  
AGAAGAGTGC GGCGGGCGGACGGAGAAAACAATCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG  
CCGCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG  
GCACCTCTGGACAGCCCAGGATGCTGTTGGCCACCCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG  
ACCGGATTATTTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA  
GGCCCCCTGGTCCGGGACAGCCGCACCTCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG  
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG  
AGTTTTAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCTCCCTGCTTGAATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT  
CTTGCCATTGGCTGTGAGACCCCATGATGGCGGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG  
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTACCCACTTCA  
GCAATGGCAAGGCTGTCACTGTGAGACACTGTCTGGCCAGGCTGTTGTGCTTACCACACAGTTGCTTGGAGCA  
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCCTGTGGCTTAGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGTGGCACTT  
TGCTGCCACAGCCTGTACTGCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTGCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATACAG  
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTCGCACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGACGACAGCAGGCACCCC  
CTTCTACGGGCAGCTCATTGCCAGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA  
ACTCAGTGCTGGGCAACCTGCGTTTCTGTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG  
CCCGCGTGTGTCAGCGGGGCGCTTGTATGCGACGCTTGTACGCCGTCTCCGCCGCTGGGGCTTGTCCCTCGAA  
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCTTGGAGGCCCTAGATG  
GTGGCACAGGTCCAGCCCGTGGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA  
AGGCTCCCCTCCCCTCTGCTAGCACGTCTCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC  
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC  
CAGGACCAACCCGGAGCCCCCTGGACCCCAACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCTCC  
ACCACTTCCCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCCTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT  
TCACCACACCTGCTCCCCACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA  
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG  
CTCACAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA  
GGAATCATACATCTC

09978192-101501



## **FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCGDVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVLTLEDFYGVFSSPGYTHLASVSH PQSCHWLLD PHDGRR LAVRFTALDLGFGDAVH  
VYDGP GPP ESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWD CADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTF CADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWD CS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGR LMRRLVR  
RLRRWG LLPRTNTPARASEARSQVTPSAAPLEALDGGTG PAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRL LPSLGPPGPTRSPPGPHTAV  
L LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

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TOSTOT 25782660

## FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

09978192.101501

## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSM TFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

**Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

09978192.101501

## FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTTATNATCGCACAAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACCTTGTGACAGCAGTATGCTGTNTTGCCGAC

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T05T0Y" 26T8X660

## FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGCGCTGCTGCTGC  
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCCGACGGCTTGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATAACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTTCTG  
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC  
CCATGATGGGGGCCCGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATTGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

09978492-101501  
TOSTOT-2672660

## **FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPATPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDLTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR  
LPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSRFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIIVLLLLLPFRC  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

09978192-101501

## FIGURE 74

CGCCTCCGCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG  
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGAATTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCCACTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAA  
AAAAAAAAAAAAAAAAAA

09978192.101501

## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTYAAHPGPVNSELFRLRHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAHRLWEASKRL  
AGLGPGEDAEPDEDPOSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP  
EIQLS

**Important features:**

**Signal peptide:**

amino acids 1-16

**Glycosaminoglycan attachment site.**

amino acids 46-49

**Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

09578192-101501  
TOSTOT-2518/650



# FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG  
 GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC  
 CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGAC  
 CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT  
 CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
 TTTACTCTGGAATGTGGGCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
 GCCCTCCAGCCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
 ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGTTTCCATCCAGGAGCCC  
 CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTGAGCTGGAAAATGTGACACTGCTGAACCCGGAT  
 CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA  
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
 GGCTGGCAGAGCGCAGAGCTTGGAGGCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC  
 CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGAAAAAGTGCCAGTGCCCCACCTCAGGAA  
 GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC  
 ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAAGTGGAGTGTAGTTGGTGAGCT  
 ACCCAGCTGGAAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCT  
 GGGGAGCCCCAGTAGACCTGTCTGCCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCCAGTGAGCAT  
 GGTCCCTGGACCTTGGAGCAGCTGAGGGTACCTTGAAGCGGCTGAGGTGATTGCCACCTGCGGTGTTGCACTC  
 TGGCTGCTGCTTCTGGGCACCGCCCTGTGTATCCACCGCCGCGCCGAGCTAGGGTGCACCTGGGCCCAGGTCTG  
 TACAGATATACAGTGAGGATGCCATCCTAAAAACACAGGATGGATCACAGTGAATCCCAGTGGTTGGCAGACACT  
 TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCCTCAGCAGTGGCTGGGGGCGGATGCCCGG  
 GACCCACTAGACTGTCTGCTCCTTGTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCTGCTTCCAGACACC  
 AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCAGGTCCCAGCT  
 GTCAGGCGCCTCCCACCCAGCTGGCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGCAGG  
 GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCTGCAGAGGCTTGGAAAGGCCAAAAAGAAGCAGGAGCTGCAGCAT  
 GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCC  
 AAGAACCTTTCCCAAAGCCCAGGAGCTGTGCCCAAGCTCTGGTTGGCTGGCGGGCCCTGGGACCCGAAACTCAG  
 AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC  
 CTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCAGCTTCCAGTCGCCTGTCC  
 AGCTCCTCACTGTCTATCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
 CTCAGTGAGGGTGAGGAGACTCCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCCTTCAACCCCCACCACTAT  
 GGGTACATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG  
 GGAGTCTTGCTGTGCCCCACCTCGGCCCTGCCCTACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC  
 TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCCTCCGATGGCTCCTTCTCGCTGAT  
 GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC  
 GTCTTCATAGATGCCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCTG  
 TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGGCTGGGAAGGGGGATGCCTCCC  
 TGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCAGTCCACTGTGATGCCAAGGCTGGTGCTTCTCCT  
 GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG  
 ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG  
 TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA  
 ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCACAGGTTGTTTTGGC  
 CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT  
 GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCT  
 GGGCCCCCTCCTTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAAGAAAATAATTATGAATGCCACTG  
 AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG  
 TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT  
 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09978192.101504

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGPGRPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP  
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAGEPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYSSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLL PDTST  
FYGSLIAELPSSTPARPSPQVPAVRRLLPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPPAPLPFHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

# FIGURE 78

CTCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCTCCTCCCTCCCCTTCTCCCAC  
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAGCTCAGCAAACCCAGCCCC  
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCCCTCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTTGGTGTGCTGAGCCTTCTGTGAGC  
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGAAGTGCAGGAGGAAAAGGAAGCC  
 CTTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTCCA  
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC  
 CTCATGCCCAGTGTGCGACCCCTGCCTTCCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTCTAACAATGCCAGTGAAGTGTGCACTTGAAGTTTGAAGGGCCAGTGGGCCTG  
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG  
 TCCAGGCCTTGGTCAAGTCAAGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
 TTGCCTTTNCCATTGCCCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
 GCACAACTACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
 GCTGCCCAGGCTGGAGTGCAGTGGCAGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT  
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCAGTGTGGCCAGGCTGGTCTTGAACCTCCTGAC  
 CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAACTTGAAAG  
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT  
 TATTTTCGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
 TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

09978192-101501

## **FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLILVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIRDSTRQELSLIVTLWNLTLQDAGEYWCGVEKRGPDSELLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD  
VISMPPLHTSEEELGFSKFVSA

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 248-269

#### **N-glycosylation site.**

amino acids 96-99

#### **Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

#### **Ig like V-type domain:**

amino acids 13-128

09978192-101501  
TOSTOT-26T8660

## FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGGCCAGCTGGGATCCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTCAACAAGCGGTTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

0978192-101501  
FOSTOT 2678/660

## **FIGURE 81**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNPNLKDTVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGPDF

**Important features:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

09978192.101501  
TOSTOT 26T82650

## FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCCGGGCGGCACCAATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAC TGCTCCACAC  
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACGAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGCGGTCTCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCACCTGGTGCTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGAGATTGCACACGTGCCGATTGACCGCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCTTTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTCTC

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

0978192 101501  
T05T01" 25T2660



## FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGCTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAATCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAATGTGTGCATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAATGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAATGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

09978192 101501  
105101 26182660

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGSSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR  
ELRERVTOGLAEAGRGREDVRTELFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

09978192 101504  
TOSTOT 2612/650

## FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAAGTGGAGCCTCATTGGCCGGCCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCGGCCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTACGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC  
CAGCCCCGACTGGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTTCGTCTTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGCAGCCCCTGGGGCCCCCGG  
GAGCCATGGGGTGTGCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG  
TCCAGGGGCCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 87**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWKKNQYVSNGLRDFEAERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWVGVDSLDLDCGDRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA  
NNGSPCPELEEEAECPDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

TOSTOT"2618/550

## FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAACCTTTGTTTGGAAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTCAATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT  
TAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTTAAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAACGGGAACTCTTAGCAG  
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTGG  
TACATGTGTTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTCT  
TCCACAAAAA

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## **FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGKTGNFSLLSFGEAEAEAEAEAEAEVNRVSQSMKGKSKSSHDLKDDPHLSSVPV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAI AETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQSDTTFEIIDPRNPVNKRREESKKLMREKKERR

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

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TOSTOT 26182660

# FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCTGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
 CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTGCGCTTGCTGACGGCGTCG  
 AGCCCTGGCCAGACATGTTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
 GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTCCTTCCTTCGGAACGGGAACGTCTAGCAA  
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
 CTCCTTCAAGTGGTTCCTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
 GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC  
 CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT  
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAA  
 GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAG  
 TGCAGTGGCAGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGC  
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG  
 ATGTACGTGACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
 CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC  
 GAGAAAGTGGTGCTGGTGTTCCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA  
 CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCCGCCAGTCCGGCG  
 GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
 CATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAAC  
 GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
 TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT  
 ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCAAGCTCAAGGAGAAGAAGATGGC  
 TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
 TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
 TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT  
 CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC  
 CCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGCTCAACCTTGTTCCTGTCTGT  
 TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA  
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
 TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

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## FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPPFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLVNYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTLEFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPPDD  
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMD  
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Carboxylesterases type-B serine active site.**

amino acids 312-327

#### **Carboxylesterases type-B signature 2.**

amino acids 218-228

#### **N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

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## FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
 GCTGTCTCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
 AGTCAGTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA  
 CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
 CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC  
 GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACCTGCTCCTTGGTGATCAGAGACGCGCAG  
 ATGCAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT  
 CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCAGGACC  
 ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
 GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTACAGTGACAACAC  
 GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT  
 TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG  
 AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG  
 GGTGAAGGCTGGGGATTAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC  
 AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTTCCAA  
 GCAAACAGGACAGTCTTGGAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA  
 AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA  
 GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGTCTTGAGCTGCCTCGGGTT  
 CAAGTGGAGCACGAAGGAGAGTTACCTGCCACGCTCGGCACCCACTGGGCTCCAGCACGT  
 CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG  
 CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG  
 ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC  
 GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA  
 AAGCCACACCAAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG  
 AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC  
 CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA  
 GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC  
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
 GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT  
 CTCTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC  
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGGGAGTTGAGACCAGCCTG  
 GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG  
 CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
 AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA  
 TCTCAAAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA  
 AGGTGGGTGGATTGCTTGAGCCAGGAGTTGAGACCAGCCTGGGCAACATGGTGAAACCCC  
 ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT  
 CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
 TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG  
 TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA  
 ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCTCACTGCTACACTCCT  
 GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCA  
 AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA  
 GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT  
 TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAAA

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## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVEEMSTRGRFQLTGDPKGNCSLVIRDAQMQDESEQYFFRVERGS  
YVTYNFMNDGGFLLKVTVLSTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYT CRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPQVRPRPEARMMPKGTQADYAEVKFQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 399-418

#### **N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

#### **Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

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"POST" 26782660

## FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGCTGTTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGCTTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTCTATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTCGCAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAAA  
AAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTTATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA  
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT  
TTACTTTAATCTATCTGTAGAAGACACTAACAAATTCAGTTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTCATTATGATCATA  
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGA  
GAAAAGTGAAGATTTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTTTACCATCAAAATTTTTTAAAAGTGCTAATGTGTATTGGAACCAATGGTAGTCTTAA  
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTTAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG  
TAGGAAGATATTTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAAATTTAAAGGAGCAAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT  
TTAAA

## **FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL  
LYSL LQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS D  
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHHFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKT TSAEIRSLY  
RQSLQVGPD SAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 597-617

#### **N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

#### **Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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TOSTOT-26182660

## **FIGURE 96**

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAAGTCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCGCAAACATTTGACATTATT

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105101 26182660

## FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCAATGGCCAACGCGGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCTTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCCTATGCCGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCATGACCCAGT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACCACAGAGGCCAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA  
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA  
ATATAGGAGGGAAGATTTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA  
ATAGACAGTAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAAT  
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCTGCC  
TTATATACATATGTAACAGTCAAATATCATTACTCTTCTTCATTAGCTTTGGGTGCCCTTG  
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT  
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA  
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
AACACAACCTTTATTGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAACT  
ACCTTTTTGTTCCTTAAATTGATTGTTTTTCCAAGTGTAATTATCATGCGTTTTTA  
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
CACTGCCTTCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
GTGGTTCACTGCCTTCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCTTCTCTCTCTACCAGTCTATTTCCATTCTTTTCACTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAACAACTGCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA  
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT  
ACTAAGGGAAAGAATTGAGGAATTAACGCATACGTTTTGGTGTTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG

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## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFILAFILGWIGAIIVSTALPQWRIYSYAGDNIVTAQAMYEGWLWMSCVSQSTGQI  
QCKVFDSLNLSSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVFNARYEFGQALFTGWAAASLCLLGALLCCSC  
PRKTTSTYPTPRPYPKPAPSSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

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TOSTOT-26T8/660

## FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTCCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCCTGTCCC

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105101 2618660



## FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTA  
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

## **FIGURE 101**

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTT  
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTGCCTGCGA

## FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT  
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCTGTCCC

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TOSTOT-2518/650

## **FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTTCCTGTCCCCGAA

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## FIGURE 104

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTTGCGAACC

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## FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTG

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## **FIGURE 106**

TTCCTGGGATGGATCCGCCCCATCNCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

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TOSTOT-26787560

## FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNCGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTGCAGAA

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## FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCTCG  
ACCGGTCCCCGCCTTTTTGTAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGGCGAAGGTGGAG  
CAGGTCCTGAGCCTCGAGCCGCGACGAGCTCAAATCCGAGGTCCCTTCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTCAGTCTATGTTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
GATAAACCACATGATGTAGAAATAAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTCTTTA  
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAAGAGGTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCAATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT  
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTG  
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTAAGTGCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAAATGCATA  
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTGACAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCCCCAAAATTAAGAAAA

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## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMLOPFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE  
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLOGEVQRLREE  
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIIGKIAL

### **Important features:**

#### **Transmembrane domain:**

amino acids 224-239

#### **N-glycosylation site.**

amino acids 68-71

#### **N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

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T05T0T 26T87660

## FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCATTTTGTACATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAAATGAGC

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## **FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTA CTGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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## **FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

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## **FIGURE 113**

GGTGGCCCATTCCTGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTTANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGT  
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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105101 26184660

## FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

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TOSTOT-26TB/660

## FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC  
GGCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTTANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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## FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAA  
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTT  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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## FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAACAAGCCTGGCAGGGTCTCACTTTGTTGCCCAGGCTGGAGTTTCACTGCCA  
TGATCATGGTTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAATAATGCTGCTTTGGTTGATATTTTTCACC  
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTGTGAGTGAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCACTCTTGACAAA  
AGGTTCTTAACCAATTTCCCTTTTCAAGCAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCTCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTATGATGGAAGGACTATG  
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC  
AGAGGATTGCCGAAGGGAGGCTTCTCTTTTCACTGGACCCGGGTCAAGAATACCCACATTCCG  
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGACTATGACTATGCTCTTCTGGA  
GCTGAAGCGTGCTCAGAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA  
TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTTTGAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
GGGCTCCACCGGTTTGGGGGCTCTATCTGCGTCTGAAAGATCCAGACAAAAGAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC  
TACAACGTTGCTGTTTCGCATCACTCCCTTAAATACGCCCAGATTTGCCTCTGGATTACGG  
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACTCTGTCAATAGCATTTCAACATTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA  
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT  
AAACCTTCAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTCACTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
GGGACATTTAGTTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA  
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTTCATGTATGCATAGGG  
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGGTGCTACATTTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTTTAGATATGTCCTTTTCTAAAAATGAATAAAATTTATGAATATGA

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## **FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV  
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDSNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

#### **Glycosaminoglycan attachment site.**

amino acids 236-239

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

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T05T0T 25T8660

## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACCTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT  
ATATCTGGAAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAAA

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## **FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKQC  
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKLPVEAKLPWFKQAQEEGA AVSEEPS

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **N-glycosylation site.**

amino acids 251-254

#### **Thrombospondin 1**

amino acids 385-399

#### **von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

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TOSTOT-26T82660

## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAAC TAGCCCGCCGCTTAGAAGGCACAAATGTACCGTCAATGTGTGTCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTCATGGGCTTTTTTTCAAACCTCAGTAGAAGGTGCCCAGACTTCCATTTATTT  
GGCCTCTTACCTGAGGTAGAAGGAGTGT CAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTT CAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

## FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEEAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSR SKLANILFTRELARRLEG TNVTNVNLHPG  
IVRTNLGRHIHIPLLVKPLENLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

#### **N-glycosylation site.**

amino acids 212-215 and 239-242

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TOSTOT-2618/660

## FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

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## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC  
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTACGGAC  
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTGGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTTCAAGAAATTCGGGACTTAGCAGAAATCACCACCTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTCTGCATTTGGGGATGTTTCAAAACCGGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCTGGAAGAACTCAAGCAATTCG  
TATTTGACTTACATTCTGGAAGAACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAAACTTG  
AAAAACAGTTTGTAAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA  
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAA

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## **FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR  
GORSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNI IYKPPGHSAPDMVYLGAMTNFDVTYNWIIQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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T05101 25184660

## FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

FOSTOT 26TB/660

## FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNNGGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTTCGTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCAATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

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## FIGURE 128

GCCCACGCGTCCGATGGCGTTCACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTAAGTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGGCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT  
GATTACCTCTGGTGTTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATTATAGGAACCTTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGT  
GCAATACAATAAACTCTGAAATTAAGACTC

## **FIGURE 129**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Type II transmembrane domain:**

amino acids 11-31

#### **Other transmembrane domain:**

amino acids 57-77 and 123-143

09978192.101501  
T05101.25182660

## **FIGURE 130**

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCTTGTA TACTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

## FIGURE 131

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT  
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAATTCCACTCCTCATAGAGCTTTTAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAATAAAGTTACTCAAATCTGTG

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TOSTOT"26T82660



## **FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA  
CQLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACH  
LGCQNQLPFA  
ELRQEQLMSLMPKMHLFPLTLVRSFWSMMDSAQSFITSSWTFYLOADDG  
KIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGLRCLSL  
NSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLV  
VVRSKTEDHEEAG  
PLPTKVNLAHSEI

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 241-260

#### **N-glycosylation site.**

amino acids 90-93

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T0510T-2518/660

## FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATCCCAATCTGATGAGCAATATGCTTGCCATCTTG GTTGCCAGAATCAGCTGCCATTTCGC  
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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TOSTOT"26T8260

## **FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAAC TGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCG  
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

09978192-101501  
TOSTOT-2618/660

## FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTTGATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTGAGTCCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACTGTTTTAAGCCAC  
AGACAATTAAGAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA  
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCCTTTG  
CATTTTGATGAGAATTCATTTTTTGTGTTGGGATAAAAAAGAAGCACACAACTAAAGGAGGA  
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA  
AATAGTATCATTATTCACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT  
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

09978192.101501

## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLSDYFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVDPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAF  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSKVLPFFERPDLQFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTOGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

09978192 101501  
TOSTOT 25782660

## FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAGAGCATTTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTTCTTTGCATTTTGTATGAGAATTCA  
TTTTTTTGCTG

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TOSTOT 2518/660

## **FIGURE 138**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA  
AATAATAATAATAATAAATTTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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"26 FEB 66"

## **FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Cell attachment sequence.**

amino acids 70-73

#### **N-glycosylation site.**

amino acids 98-101

#### **Integrins alpha chain proteins**

amino acids 67-81

09978192-101501  
TOSTOT-25182660



## **FIGURE 140**

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAAC TCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

09978192.101504

## FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
**AATGC**CAGACTTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTGTGGCTTCATGCTGATCCTTGT  
GGTCTGTGCCACTGTTCTGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCTTCCCAGACACCTTGAAAATAACCAATTCACCCAGAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTC**ATAGG**TTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC  
ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
TGTGTTGTAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAA

09978192.101501

## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

FOSTOT 26T82660

## **FIGURE 143**

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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F05101.25182660

## FIGURE 144

CCCACGCGTCCGCCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTTGGGGAACCTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGC GGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACCTCAACCAGGAACTCTACGGGAATTTAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE  
TVTWILIDRALNITSLOMHSRLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 177-199

#### **N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

09978192.101501

## FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC  
GTTTCGTGTCCCCGCCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA  
GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTCCTGCCATTTCTTCCAGGTTGAGGGAGC  
CGCAGAGGCGGAGGCTCGCGTATTCTGCAGTCAGCACCCACGTCGCCCGGACGCTCGGTGCTCAGGCCCTTC  
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCGGGCGTCCGGTTTGGCT  
CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA  
ATCCTGAGGTCAATCATTATGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACCACAGTGCTGTTTATGGCTAGA  
GCAATTCAGCCATGGTGGTTCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT  
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA  
TCTGCAGAACTCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT  
TTGGGAGCACACTGGGGAAGATATAGGCCCGGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT  
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA  
CAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCTATAACATGAACATCTGGGGGCG  
ATATGGCCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTGGAGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG  
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAATGTCCAAATTGTTTCT  
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAATGTCCAAATTGTTTCT  
TGTGAAGTAAGATTAAGAGATCAGTGCAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTGGAT  
AGTAAAGCTAAAGTTATTGGCAGTGATCATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT  
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCAAGTCCAATAGA  
AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTACAGTCTCTAAAGTAACAGTTTCAGGCTGTG  
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTATAAGCCTGCTTACATTGCCCCAAGAGTATACTGTCT  
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAATTGGAACCTGAGTTTATTCTGATCTGTCCAGTATC  
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA  
AAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT  
AGAGTGTGTTGCTGTTGTGTGAAACTGAATACTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA  
ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTTCAGCCCAAAAAGGTGCCAAATGCATA  
TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG  
TTTTAGAAATCCTGTGTTAAATATGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT  
GTTCTACGTTTCATATATTATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
GCCCTCAGAAAATCATCTAGTGCAATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC  
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC  
TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC  
CAAATGAATCTGTGTTAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT  
ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA  
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT  
GAACAAAGATGAACATAATGTATTACATTACCATTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATA  
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACATAA  
AATCTGTAAATGTTAGTTTTGGTAATTTTTTTCTGCTGGTGATTTACATATTAAATTTTTTCTGCTGGTGGA  
TAAACATTAAATTAATCATGTTTTCAAAAAAAAAAAAA

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLC  
HNMNIWGQIWP KAVYLV CNYS PKGNWWGHAPYKHGRPC SACPPSFGGGCRENL CYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR  
YEC PAGCLDSKAKVIGSVHYEQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSES LQNPPGGKA FRV  
FAVV

**Important features:**

**Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

09978193-101501  
TOSTOT-26T8/660



## FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCG  
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCCGGA  
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCCCTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCTTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGCTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT  
GGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAA

0938192.101501

## FIGURE 149

MSLLPRRAPPVSMRLLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

09978192.101504  
TOSTOT" 26TB/660

## FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTTACCCCCGGTCTGCGTCATGTTAAACTCCAATGTCTCTCTGTG  
GTAACTGCTCTTGCCATCAAGTTCACCCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG  
CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA  
TGCCTCACCCCCCACTGGAGAGAGGCGGTTTCAGCCCCCAGAACCCCGTCTCCTGGACTGGCATCCGAAATAC  
TACTCAGTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT  
TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTAAACATCTACGT  
GCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA  
TATTATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA  
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTTCATCGTGATCACCATTAACTACCGTCTGGGAATACT  
AGGGTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG  
GATTGAGGAGAATGTGGGAGCCTTTGCGCGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC  
CTGTGTGACGCTGTTGACCCGTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTAGAGCGGCACCGC  
CCTGTCCAGCTGGGCAGTGAACCTACAGCCGGCCAACTACCTCGGATATTGGCAGACAAGGTCGGCTGCAACAT  
GCTGGACACCACGGACATGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC  
GGCCACCTACCACATAGCCTTCGGGCGGGTGATCGACGGCGACGTTCATCCAGACGACCCCGAGATCCTGATGGA  
GCAAGGCGAGTTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTCTGGACGGCAT  
CGTGGATAACGAGGACGGTGTGACGCCCCAAGACTTTGACTTCTCCGTGTCCAATTCTGGACAACCTTTACGG  
CTACCCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCC  
GGAGACGCGGCGGAAACCCCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCCGTGGCCGCGGACCT  
GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCCAGCTG  
GGCAGATTCCGGCCCATGGTGATGAGGTCCCTATGTCTTCGGCATCCCATGATCGGTCCCACCGAGCTCTTCAG  
TTGTAACTTTTCCAAGAACGACGTTCATGCTCAGCGCCGTGGTTCATGACCTACTGGACGAATTCGCCAAAACCTGG  
TGATCCAAATCAACAGTTCTCTCAGGATACCAAGTTCATTACACAAAACCCAAACCGCTTTGAAGAAGTGGCCTG  
GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC  
AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCCTCATTTCACAACTTGAAACGAGATATTCCAGTATGTTTCAAC  
AACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCACCCCGCGATCTCCCGCCAAGATATGGCC  
AACCACAAACGCCCAGCAATCACTCTGCCAACAACTCCCAAACACTTAAGGACCCTCACAAAACAGGGCCTGA  
GGACACAACGTCTCTCATTGAAACCAAACGAGATTATTCCACCGAATTAAGTGTCAACATTGCCGTGGGGCGTC  
GCTCCTCTTCTCAACATCTTAGCTTTTGCGGCGCTGTACTACAAAAGGACAAGAGGGCGCCATGAGACTCACAG  
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT  
GAAGCAGCTGGAACACGATCACGAGTGTGAGTCGCTGCAGGCACACGACACACTGAGGCTCACCTGCCCCGCGAGA  
CTACACCCCTCACGCTGCGCCGGTCCGACAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA  
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAAACACTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA  
CGGACATTCCACCCTAGAGTATAGCTTTTGCCCTATTTCCCTTCCCTATCCCTCTGCCCTACCCGCTCAGCAACAT  
AGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCACT  
GACTTAAGACAAAATGCAAAAAGGCAGTCATCCCATCCCGGCAGACCTTATCGTTGGTGTTTTCCAGTATTAC  
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTTAAAATAACTGCTTTAAGATCTCTACCA  
CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCACACGTTCATGGAAGCAGCT  
GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC  
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCAGCACATGGAGCTGTAATCCAG  
AGAGAAGGAAACGTAGAAATTTATTATTAAGAAGTGGACTGTGCAGCGAAATCTGTACGGTCTGTGCAAGAG  
GTGTTTTGCCAGCCTGAACTATATTTAAGAGACTTTGT

## **FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLEPIWFTANLDTLMTYVQDQN  
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEGDVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYPDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPYV  
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQPVQD TKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTE LSVTI AVG  
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

09978192 101501  
105101 26182660

# FIGURE 152

GGGAAAGATGCGCGGCGACTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGT  
 CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTTGTTGGGGTCTGGGCAGGGGCCA  
 CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTGGAAGCC  
 CTACCAGGGTGTGGGCACAGGCAGTTCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
 TGACCCAGTATATCCGCCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
 GTGCCATGTTTCTTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAA  
 GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
 CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
 GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
 CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
 GCAATCTTCATTACGACACCTTCTGGTGATTGCTACGTCAAGAGGCATTTGACGATAATG  
 ATGGATATTGATGGCAAGCATGAGTGGAGGACTGCATTGAAGTGCCCGAGTCCGCTGCC  
 CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
 TTTCTTGAAGTTGTTTGAACGTGACAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGA  
 GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
 CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA  
 TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
 GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCCTG  
 GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
 TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTCATGGTTGTGCATGGGGACATCTAACT  
 CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
 TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
 AGAATTTCATAGCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG  
 AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTGCTGGGTT  
 TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT  
 TCTTCCCTGCCTTACCTTCTTTCACTCCATTCAATTGTCCTCTCTGTGTGCAACCTGAGCTG  
 GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCTGGGGCTGCAGAACACACCTGCGTTTCAC  
 TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
 GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
 AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
 GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTGATGTG  
 GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
 TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT  
 GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT  
 TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT  
 CACTGTCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA  
 TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
 AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT  
 TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
 ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

09978192.101501

## **FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQ GALWNRVPCFLRDWELQVHFKEHGQGKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY  
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329

09978192-101501  
TOSTOT-26182560

## FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT  
CTGATGGTGGGTCTGTTAACTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT  
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTAATTAATGCCTGCAGTCT  
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT  
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCCGACCCTGTGACGGAGCCCCCTGTGA  
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCCC  
CGCATCATTTTAAAGCTGGTCTCAGTGCATGTGTTTCATTGCCCACGGAGACAGGTACCCACTGTATGTTCATTCCCA  
AAACAAAGCGACCCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA  
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTGAAAGCCCCCTTGAACCTCTTGCCTCTTTACCCAAATCACC  
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA  
TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA  
GCCCGACCCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA  
GGCACCAGCCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACAGTATCTGAAAAAGGAGC  
AGCGTCGTCAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG  
ATGTCCCCAACAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCCAATGTGAGCT  
TTCCCTGTACCAAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAAGAAATTTGACTTCGGGTATTCTCTCTGGGTGCCACCCCATCTGAACCAAAACCATCG  
GCCGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT  
CACCAGTTCTCAGTGCTTGGGCTTTTCAAGGCCAGGTTCCCAAGGTTTGAGCCAGGTTGATCTTTGAGCTTT  
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGATTCTTTACAATGGCGTCGATGTCACTTCCACACCT  
CTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA  
GGGACATGTTTTGTAGCCCTGGGTGGCAGTGGTACAAAATTATTATGATGTCATGTACAGGGAAGGATTTCTAAAGG  
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTAC  
TAAGGGTAGAAGATTATTGCTTTTAAAGGCTAAATATTGTTTGTGGGAACACAGATGGTTGGGGTTGAACAGT  
AAGCACATTGCTGCAATGTGTTACGTGAATTGCTTGGTACAAAATGGCCAGTTCAAGAGGAATAGAAGGTACTT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC  
TCTTCTGGCCTGCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTAACTCTTAGACATT  
TTTACCTTGTCTTGTGTTAAGAAATTTCTGAAGTGATTATCTAAAATAAAGGTTGGCAAACTTTTTCTGTAAAGG  
GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTAACTACTCACTCTGT  
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA  
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC  
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCTCCAGTAACCTCTGCTAGAAACA  
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA  
AACTGATTAGAAGAATACTTGATGTTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTTGT  
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTATAGTTTAGGAAAATATT  
TTCTAAGACCAGTTTTAGATGACTCTATTCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA  
ACTGGATTCAATTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTAAATGCGTTTTTGA  
AGAATTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG  
TGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGAAGTGAAAGTGAGATTCTCTGTTGTATCGGCATTCC  
AACTTTTTCTCTTTGTTTTTGTCCAGTGTTCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

## FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMDPVTEPPVTDPVY  
EALLYCNIPVAERSMEGHAPHHFKLVSVHVFIRHGDYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSF  
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYDACHREGF

**Signal sequence:**

amino acids 1-18

09978192-101501  
TOSTOT-2518/550



# FIGURE 156

AAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA  
GCTATTTAAGAGATAAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCTGAAGCACAAAGCAGAT  
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT  
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT  
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG  
ATGCACCCAGATACGCTATTTCAGTTCCGGAAGAGCTGGAGAAAAGGCTCTAGGGTGGCGACATCTCCAGGGACCT  
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCAGAGGTAGGACGCGAGCTTTTCGCCCT  
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG  
TCAATTTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
CGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT  
CCCTCTACCCACGCCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA  
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCTGGACCG  
CGAAGAAAAGCTGCTCACCACCTGGTCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG  
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCAGCGTTTGTCTCAGCCCGAGTACCGCGCGAGCGTTCC  
GGAGAATCTGGCCTTGGGCACGCGAGCTGCTTGTAGTCAACGCTACCGACCCTGACGAAGGAGTCAATGCGGAAGT  
GAGGTATTCTTCCGCTATGTGGACGACAAGGCGGCCAAGTTTTCAAACCTAGATTGTAATTGAGGACAATATC  
AACAAATAGGGGAGTTGGACCAGGAGTCAAGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA  
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCGAGAAGTGGTCTCACCCTCTCT  
CGCCAGCTCGGTTCCCGAAAACTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAATGACCAAGATTCTGA  
GGAAAACGGACAGGTGATCTGTTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA  
TAGTTTATGTCACAGACATAGTCTTGGATAGGGAAACAGGTTCTTAGCTACAACATCAGAGTGACCGCCACTGACCG  
GGGAACCCCGCCCCCTATCCACGGAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCCGCCGGTCTT  
CCCTCAGGCCCTCCTATTCCGCTTATATCCAGAGAAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
CGACCCCGACTGTGAAGAGAACGCCAGATCACTTATTCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC  
GTCCTACGTGTCCATCACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA  
CTTGCAAGTGAAGTGATGGCGCGGGACAACGGGCAACCGCCCCCTCAGCAGCAACGTGTCTGTTGAGCCTGTTCTG  
CTGGAGACCAGAACGACAATGCGCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCT  
GGCTCCCCGCTCCGCGAGAGCCCGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC  
CTGGCTGTCTTACCCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG  
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC  
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGGCAG  
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG  
CGTCTTCTCGGCCTTCGTCATCTTGTCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTGCAGGC  
TTCAGGAGGCGGCTTGACAGGAGCGCCGCGCTCGCACTTTGTGGGCGTGGACGGGGTGCAGGCTTTCTGTCAGAC  
CTATTCCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACCTGATCTTCCCCAGCCCAACTATGCAGA  
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTCTGTCAGGTGATTGGGTATTTCTAAAGA  
CAGTCATGGGTAAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTTTAAATTGCTCTGTCTCCCAAGC  
TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCCTAGGCTCAAGCAATTATCCCACCTTTGCCT  
CCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT  
CTATCTATCTATCTATCTATTACTTTCTGTACAGACGGGAGTCTCACGCCTGTAATCCAGTACTTTGGGAGGC  
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGGAGCCAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA  
AAAAATACAAAATTAGCCGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG  
AAACTCTATCTCA

105101 26187660

## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRY SFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYYS LVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVS LVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN  
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVA VDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVT LTVAVADSIPQVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILL LALRLRRWHKSRL LQASGGGLTGAPASHFVGVD  
GVQAF LQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNC SVSQAGVQRYDHSSLRPQT PRLKQLSHLCLRCNRDYRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

05978192.10504

## **FIGURE 158**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTCTGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGGTGGCAACTGGGTCCTT  
ACAGCTGCCCCTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT  
CTGGTTC

09978192-101501

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGSDDPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

09978192-101501

## FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCCTGCGCGCCCCGGCCCCG  
CGCGCCGCCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCG  
GCCCCGCGCCAGGTGAGCGCTCCGCCCCGCGGAGGCCCCGCCCCGGCCCCGCCCCGCCCCG  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCCATAAAAC  
ATTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCGCCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGGGCGGTAGCGGCGGCGCCTGGA  
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGC  
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCGCCTACACACGCTGCACCTGGACCGC  
TGCGGCCTGCAGGAGCTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGGCCATGTGCACCCGCATGCCTT  
CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCCCACTCTGGGCCTGGCTGCAGAAGTTCGCGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGGTG  
ACAGCCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCTTCCCTGATGGACGCCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA  
AAAA

09978192.101501

## **FIGURE 161**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLHLHQNVAHVHVPFAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Leucine zipper pattern.**

amino acids 135-156

#### **Glycosaminoglycan attachment site.**

amino acids 436-439

#### **N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

#### **VWFC domain**

amino acids 411-425

09978192.101501  
TOSTOT.2618/660

## FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC  
 AGTCCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGAGAGGCCAGCGGGA  
 AGCTCATTTTGCAGACAAAGGCAAGTCTTTTCTTTTCTCTTTTGGGCTTATCTCTGGCG  
 GCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC  
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGTTAGGGTTG  
 TTTCCAGAGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT  
 GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
 GTTGCTAGAGAGTCCCTTCGAGTTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG  
 ACTACGTTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
 TATAATCAGCCCCAACTCCTATTTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT  
 ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
 CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
 CCTGGATGTCAACGATAATGCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
 AGGACAGTCCGCTAGGCTTCTGTTGTGAAGTCTCTGCCACGGATGTAGACACAGGAGTC  
 AACGGAGAGATTTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
 CAATCCCTTGACAGGAGAAATTGAACATAAAAAACAACCTCGATTTGAAAAACTTCAGTCTCT  
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
 CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
 ACCTGAGAACGCGCCTGAAACTGTGGTTGCATTTTTCAGTGTTTCAGATCTTGATTGAGGAG  
 AAAATGGGAAAATTAGTTGCTCCATTGAGGAGGATCTACCCTTCTCTCTGAAATCCGCGGAA  
 AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT  
 CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
 TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTCTGTC  
 CGCGAGAACACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG  
 CACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCCCTCACAT  
 CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCTGCCCTCAGGTCTCTGGACTACGAG  
 GCCCTGCAGGGGTTCCAGTTCGCGCTGGGCGCTTCAGACCACGGCTCCCGGCGCTGAGCAG  
 CGAGGCGCTGGTGCCTGGTGGTGGTGGACGCCAACGACAACCTCGCCCTTCTGTCTGTACC  
 CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGGAGCCGGGCTAC  
 CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA  
 GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCTGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTGGTCAAGGAC  
 AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
 CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCCAGGCCGACTTGCTCACCG  
 TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCTGCTCTTCTCTTTTTCGGTGCTCCTGTTT  
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTTGGTGGCCGA  
 GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC  
 AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTGAAGCCGATT  
 ATCCCCAACTTCCCTCCCAAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
 TAACTTTGGGTTCAATATTCAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
 TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
 TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
 CCTGGTTCTT

09978192-101501

## **FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTPCVLRQVLLSPFEFFQAEQV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLVDNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDGTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLKSAENFYTLTLLTERPLDRESRAEYNITITVTDLGTPLITQ  
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 685-712

#### **Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

#### **N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789



## FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

09978192 "101501"

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRPRPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

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TOSTOT.26T82660

## FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC  
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCA<sup>^</sup>ACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCCTGAAAATAAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCCAACCGAATCTTGTAAGAAATATTCAAACATAATA  
AAATCATGAATATTTTAA

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## FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGP GSLLLLFLASHCC LGSARG LFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHS LCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSE RDLKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREFKRISRSIRKLQC

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

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TOSTOT"26T8/660

Demographics		Psychiatric History		Substance Use		Current Status	
Variable	Value	Variable	Value	Variable	Value	Variable	Value
Age (mean)	35.2	Previous hospitalizations	1.5	Alcohol use (days/week)	2.5	Current symptoms	3.5
Gender (male/female)	15/15	Family history of psychosis	5	Drug use (days/week)	1.5	Medication adherence	2.5
Education (years)	12.5	Previous suicide attempts	2	Smoking status	10/No	Side effects	1.5
Employment status	10/5	Current psychiatric treatment	1.5	Exercise frequency	2/No	Quality of life	2.5
Marital status	10/5	Duration of illness	5	Stress management	2/No	Social support	2.5
Living situation	10/5	Previous self-harm	1	Religious/spiritual beliefs	2/No	Healthcare access	2.5
Legal history	10/5	Current social functioning	2.5	Personal goals	2/No	Insurance status	2.5
Financial status	10/5	Previous trauma	1	Future plans	2/No	Compliance with treatment	2.5
Health insurance	10/5	Current support system	2.5	Overall well-being	2.5		

GTGGAGGCCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTCTGCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTGTCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACC  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATAACGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCCACCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPLV  
KKGEDIPMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGILIMLMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

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T05T0T"26T2/660

## FIGURE 170

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCTGAAGTGGACCAAC  
TAGTTCCTCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCCCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGCGAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGCGGTAAGCAATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAAGTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCCGCTT  
CCAGGTGTTGCAGCTGCCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACAGCCACGGTTTCCCAAAGGCGAGCAGGA  
TACACCCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCCTTGGATGTGATTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTTGATCTGGTGTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG  
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAC  
GACCGCCACAGACCCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCCTCAGAGGT  
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAAGCCGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCCC  
TAACACCCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCCTTGGATGTGATTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTTGATCTGGTGTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG  
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAC  
GACCGCCACAGACCCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCCTCAGAGGT  
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAAGCCGATCCCCCTGGACAGGTCATTCTGCGTGCACCTCTAGACTATGAAAAGAACCC  
TGCCTACGAGGTGGATGTTGAGGCAAGGGACCTGGGTCCCAATCCTATCCAGCCCATTGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCAGTCACATGGGCCTCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTTTATTGCTCTTGTGTCATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGCCCAATATACCCTCACTGTGTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTGAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA  
AGTCTCCAGCGGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCAAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAACATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTGACGCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCTTCCACAGGCCACCTGCTGGTGGC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT  
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAATGGAGAGCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCCACCTCTTCACTCTCAACCCTCATACGGGGCAGCTGTTCTGTCATGTCACCAATGCCAGCAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTTGTCAACAGTGTGGACACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTGGGTTGATCCTGGCTTTGTTTTCATGTCCATCTGCCG  
GACAGAAAAGAAGGACAACAGGCTTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAAACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCAAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCCTGCAGGCCCCCTT  
CCACCTCACCCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGT  
GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCAGGCAGAGGAATGCCCTCCCGGAGAACCTGAACTTCC  
TGAGACCCAGGCGAGTGAGGAAGCCCCACAGAGGCCACAGCCTCCTCTGCAACCCCTGAGACCGGACGACATCT  
CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCCCTTCGCGGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTCAAGCAATCTCCAGCTGCT  
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCAAACCAAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG  
CAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCGCCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCACTGACGCTCAGGCATGAAAGTGCAAGGGACCCAGGTGG  
AAAGACGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC  
CTGGATCCCAAGAACCGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACCTCACTAGCTAG  
CGGCGGCTTGAAGACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCAGGACTAACAGCTGAC  
TGACCAAGCAGCCCCCTTGTAAAGCAGCTCTGAGTCTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT  
TCCTGGCAAACATATGTGGAGCACAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGCTGTACCCTGGGGGTGCCAGGAATGCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAA

## **FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVDLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESS  
LALAIQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNIPIAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSNLNYYEEMAGFEFQVIAEDSGQPMCLASSVSVVWSLLDA  
NDNAPEVVQPVLSDGKASLSVLVNASLGHLVPIETPNGLGPAGTDTPLATHSSRPFLLT  
IVARDADSGANGEPLYRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCQLQAPFHLTPTLTYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGS  
RSAIPDPTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEPESLPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAASGMKVQGDPPGGKTGTGEGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563



## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTTGGATTTGGGTGGCTTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTTGGTGTCTGTCAACTGCCCATACTTACATGTCTTACTTCTT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACCTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATAATCACTGAAGTCCTTGAGAACTGCAGTTCAACTTCTATACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

09978192.101501

## **FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFF  
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

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TOSTOT-2618/650

## FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTACGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCAACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

09978192 101501  
TOSTOT 26782660

## FIGURE 175

GTGTTGCCCTTG GGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCAACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTCCTC

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TOSTOT-26T8/660

# FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT  
TGGCTCCCTGCTCGTCAACTGCTCTTCTACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA  
GGAGGGCGAGCCAGGCAGCCTCTTCCGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG  
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCCGCTTG  
CCCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA  
GGAGAACCAGTGGTTGGGAGTCAGTGTTCCGAGCCAGGGGCCCTGGGGGCAAGATTGTTACCTGTGCACACCGATA  
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCCGTGCTTTGTGCTCAGCCAGGA  
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT  
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC  
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGGCACACCTGGACGACGG  
TCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGTCCCTGCCAACAGCTACTTTGGCTT  
CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA  
CAAGGGTGCTGTGGTCATCCTGCGCAAGGACAGCGCCAGTCGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG  
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG  
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGGTCACTG  
GGCTGGGATCTCCCCCTCTCCGGCTCTGCGGCTCCCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA  
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCTTTGATGGTGTGGGAAAGTCTTCATCTACCA  
TGGGAGCAGCCTGGGGGTGTGCGCAAAACCTTACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG  
CTACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC  
CGCAGTGCTCTTACGGGCCAGACCCATCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT  
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC  
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCAGGAGTCCGGGGCCAGGT  
TCCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCA  
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT  
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGGTGCCTCCAGTGGC  
CCCCATCCTCAATGCCCACCAGCCCAGCACCCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA  
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCCGCTTCTGTACCCGGGTGAGCGACACGGAAATCCAACC  
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCATGAGTGAGGCGAGCCAGTCAATGGCCCTGGAGCTGAT  
GGTCACCAACCTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT  
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAAGCCACTCTGCCTGTCCAA  
TGAGAAATGCTCCCATGTTGAGTGTGAGCTGGGGAAACCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT  
CCTTAGCACCTCCGGGATCAGCATTGAGACCAGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA  
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC  
CCAGCAACTCTTCTCTGCTGTGGTGTGGTGAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGT  
CAAGTATGAGGTCACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG  
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGG  
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGA  
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGTC  
TGAGAAGAAGAAAAACATCACCCCTGGACTGCGCCCCGGGGCACGGCCAACTGTGTGGTGTTCAGCTGCCCACTCTA  
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC  
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA  
TGCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT  
CATCCTCCTGGCTGTACTGGCTGGGCTGTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT  
CAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGGAAGACCGACAGCA  
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACTGGGGCAGCCCCCGCGGGAGGGCCCCGATGCACA  
CCCCATCCTGGCTGTGACGGGCATCCCCAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCTAGGTTCC  
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT  
GGGCTGTGGTGTGCGCATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCCACCCACAAGAAC  
TCCTCCCACCCAACTTCCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG  
TGAGAAGGGCAGGGGTGCTCTGATGCAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTCACCCGTGT  
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCTTAACTAGAGGTCGGGGAGGAGGTTGTGTCACTGA  
CTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGT  
TTCGTCTATTTATTAAAAAATATTTGAGAACAAAAA

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## FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMOKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGEWKFC  
RPGQHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGTAARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGDNLNQGFPDI AVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE  
GEAVGIKSGFGYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFYSYIAVPSSYSPT VALDYVLDADTDRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQ PSTQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSPDPAQPQADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN  
ENASHVECELGNPMKRG AQVTFYLILSTSGIS IETTELEVELL LATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVT VSNQGQSLRTLGS AFLNIM  
WPHEIANGKWL LYPMQVELEGGQGPQKGLCS PRPNILHLDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANC VVFSCPLYSFDRAAVLHVWGRLWNSTFLEEY  
SAVKSLEVIVRANITVKSSIKNLMLRDASTV I PVMVYLDPM AVVAEGVPWWVILLAVLAGLL  
VLALLVLLWKMGGFFKRAKHPEATVPQYH AVKIPREDRQQFKEEKTG TILRNNWGS PRREGP  
DAHPILAADGHPELGPDGHPGPGTA

### Important features:

#### Signal peptide:

amino acids 1-33

#### Transmembrane domain:

amino acids 1040-1062

#### N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

## FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAACAAGATGCTCAAGGTGTCAGCCGTAAGTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATAATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAGGCGCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTATGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTCACGAGAACAAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

## **FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLLRPERSRFDTSILPI  
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDYRGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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"05101" 26182660



# FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
 CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC  
 GCTCTGCCCTCCGGTGCCTGCTGCCCTGGGGCGCCGGCTTACACCTTCCCTCGATAGCGACTTCACCTTTACCCTT  
 CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCCGCTTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA  
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA  
 TCAGATGGAGTTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT  
 TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG  
 AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
 AGACTAAGCAAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC  
 AACTTTGATAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTGTCAGCCATTCAAGTTTTAT  
 ATGCTGAAGAGTCTGTTTTGAAGATAAGAGGAAAAGTAGAACTTAAAACTCCAACTAGAGTACGTAACATTGAAA  
 AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
 AAAGTAGGAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
 TTGTACTTAAGTGTGTAACAGGAATATTTTGCAGAAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT  
 TTTCTAACTTTGAAAAATTTTGCAAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC  
 AGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTGTAAATGCGGCAGTTACAAATTAACCTGTGGAAGTTT  
 TCAGTTTTTAAGTTATAAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA  
 CTTTTCTCTATTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
 AGATTTTTTATAACCAATACATTTTCAGTGAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC  
 CAAAAGCTGACATTTTTCAGGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG  
 AAATGAAGAATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTTCTTAACCTTAACTAAAGTGTAGGA  
 TTTTAAATTAATGTGAGGTAAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
 TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTTGGATAAATTCATTATTACCAGCAGTTATGAAGGAAATA  
 TTGCTAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAAACAGGAA  
 AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAAATTCACTTAAGTAGAACTATAAATAAATATCTAGA  
 ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
 AAATTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCCTGGTTTGAATTATTTTGTAAAGCAGGTACATTTTATA  
 AAATGAAGCCCTACTGTAAGTTTAGCACTGGGTGTACATATTTATTAATAAATTTTATTATAACAATTTTAT  
 TAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTATAGGATTAGAAACATAGACTCCCAAGTTTAAA  
 CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTTGAAGTCTATGGGGGTCTTAC  
 TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAAGTATGCCCCATTTATAACGTTGTTTAT  
 GACTACATTGTGAGTTAGAAACAACTTAAAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
 CTTGATGAGCAATAATGATAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
 TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT  
 ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
 AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGGCGCTGTTAAATTTGCAATGAGAAGCAAATTTACA  
 GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTCTATAAACTGTGATTAAGAATTCTA  
 CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT  
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAACGATAATTGCTT  
 TATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
 CATAACCAAAAAAGCAAACTTGTAAAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT  
 CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT  
 AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAATCTACAATATTTAACTAAGGCCCAACCGATTTT  
 CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCCTAGAGTTTGCCTCTGATATGCATTTGGATGATTAAT  
 GTTATGCTGTTCTTTTCAATGTGAATGTCAAGACATGGAGGGTGTGTTGTAATTTTATGGTAAAAATTAATCCTTCTTA  
 CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTTGTATGTCTCCTCAAATGAAGATTCCTTAT  
 GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTTTCTGAAAGTACAATAATGCACAATCAGTGTG  
 CTCAAAGTCTTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA  
 AAATTATCAAAGGAAAA

## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEY  
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL  
ILDNMGEQAQEEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

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T05T0T.2618/660

## FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTTGATG  
CTGCTTTCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACTCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC  
TTCTTTTTCTTTTTCTTCACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

09978192 101501

## FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

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T05101.26T8260

## **FIGURE 184**

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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105101 26782660

## **FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

09978192-101501

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTC AACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

## **FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIIDNYQPYPYCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGS HGLEIFQRCYCGEGLSCRIQ  
KDH HQASNSSRLHTCQRH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 256-259

#### **Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

FOSTOT-2678/650



## FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCTGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGATGGG

09978192.101501

# FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCCTGCGCCGCGG  
 CTGGGCCCGTCCGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA  
 GGGTTTGGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTGTGGAATGAAAAGGA  
 AGTATTAGAAAATGAGCTGAAGACCATTCACAGATTAATATTTTGGGGACAGATTTGTGATGCTTGATTACCCCT  
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
 TTAAATCAGAACTTGCATAAGAAAAGAGATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTTGG  
 AGTGTCCAAAACCTGCAAGCAGTAGAGAAAATAAGACAAGCTTTCAAGAAAATTGGCATTGAAGTTACATCCTGATAA  
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
 CTATTATCGTTATGATTTTGGTATTTATGATGATCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGCT  
 TGCTGTTAATCTGGAGAACTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTTCACTGCCATGATTTAGCTCC  
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCTGAATTTGGAGCTGTTAACTGTGGTGATGATAGAAT  
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCATTTTTTCGGTCTGGAATGGCCCCAGTGAATA  
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTCGAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTCTGGTATTGGCTGGCTGATCACTTTTTGTTTCAAA  
 AGGAGGAGATTGTTTTGACTTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAA  
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAACACTTTTCGGCAACACACTAGAGGATCGTTT  
 GGCTCATCATCGGTGGCTGTTATTTTTTTCATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAAT  
 AAAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTGTCTCTGCAACAGACATCTGTAGTAA  
 TCTGTATGTTTTTTCAGCCGCTCTTAGCAGTATTTAAAGGACAAGGAACCAAAGAATGAAATTCATCATGGAAA  
 GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTTACCAGCTTGGACCTCAAAA  
 TTTTCTGCCAATGACAAAGAACCAGTGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT  
 ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAAGTTTGGTACACTAGATTGTACAGTTTATGA  
 GGGACTCTGTAAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTTCAACCAGTCCAACATTTCATGAGTA  
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
 ACCCACCACCTTCAACGAACCTAGTTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG  
 GTGTCATCCTTGCCAAAGTCTTAATGCGAAGTGGAAAAGAAATGGCCCGGACATTAACCTGAGTATCAACGTGGG  
 CAGTATAGATTGCCCAACAGTATCATTCTTTTTTGTGCCAGGAAAACGTTCAAAGATAACCTGAGATAAGATTTTT  
 TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCCTGAGAAT  
 CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAAGTTCTACAAGG  
 GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGTCTCCAGAATTTGAGCT  
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA  
 AGTGGGATCAGGCGCTTCCAACTGTTAAGTTTTATTTCTACGAAAGAGCAAAAGAGAAATTTTCAAGAAGAGCA  
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAATAATTTGGAACTCTCCGAAATCAAGGCAA  
 GAGGAATAAGGATGAACCTTTGATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAAATCTGACAGATGACATCAG  
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA  
 GAATTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA  
 GACTTTGCAGGCTATAATATATGGTTTACACATGAGAACAAAGATAGAGTCATCATGTATTCTTTGTTATTTGCT  
 TTTAACAACCTTTAAAAAATATTAACAGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTAGTCCATG  
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTTAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTACGTTTTTTGGCTGACCTGAAAAGAGGTAAC  
 TAGTTTTTGGTCACTTGTCTCTCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTAAAAACACCCAT  
 GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATATGAGGAGATTCTTCATTGTTTTCTTTCTTCTCA  
 AAGGTTGAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
 AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA  
 TAGCAATTAACCTGGGCATTGTAGAGTATCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
 TGTGTTTCATGTATTTTCTGAAATTGCTTTTATAGAAATTTTCCCACTGATAGTTGATTTTGGGCATCTAATAT  
 TTACATATTTGCCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTTACATTGGGTTTTCTTTTCATAGTTTGG  
 TTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT  
 AATGATACTGTAGTTATTTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTTCAGATAAATATTGACATAATA  
 ACTGAAGTTATTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTTCTGTGTTTGTAGA  
 CTCAAAGAATCACAAATTTGTGAGTAACATGTAGTTGTTTAGTTATAATTACAGAGTGTACAGAATGGTAAAAAT  
 CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCAACTTTTTTCAAAAAAAAAAAAAAAAAA

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## **FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNPNNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDERSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP  
SLAVFKGQGTKEYEIIHHGKKILYDILAFAKESVNSHVTTLGPNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTDLTPTQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC  
QAYAQTQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRNKDEL

### **Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

09978192 101501

## FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTACCA  
AAAATCCAAGCACAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATTGAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTTACATTTTT  
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTT  
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCTTTTT  
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCTCCCTTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAA  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

09978192.101501

## FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVVFVNTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

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TOSTOT-26TB/660

## FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTTCGGTGTTCATGATCCT  
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACACACCAGCCTGCCCCGCTCGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

## **FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSF SRPHTGPPLPTPGPDRDRELT  
DSDVDEFLLDKFLSAGVKQSDLPRKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFP TKERAFDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWKRMIVLS  
GSL LHRGAPYRDPLRIPREHVHNASAH LTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFEL ENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDEDAQAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLEFGYPK PENLLRD

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

#### **TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

09978192-101501  
TOSTOT" 26182660

## **FIGURE 195**

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG  
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCAACCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

09978192.101501



## **FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQRPETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

09978192.101501  
"105101" 26184660

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCTGGCCCCTCACCAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGA  
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

09372192-101501  
TOSTOT"26T2660

## FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEFY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIavgctCIF

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 75-78

#### **Homologous region to IL-17**

amino acids 96-180.

09978192 101504  
105101 26182660

# FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAACATGGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACTGGACGCTGGTGATGGAGGGCGAGTGATGCTGAAATTT  
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCAACACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGCGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTGTTAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGGCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTTGCCAGC  
TGACACAGAGGTGGTGGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTTGTGTAAAGTATTTAT  
TTTTGTCAAATTGCAAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTTACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCTTGGGTCTTGAAC  
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTTCCATCTTCTGTAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

09978192.101501

## FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQTDSWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAESEEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 191-211

#### **N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

#### **Flavodoxin proteins**

amino acids 173-187

0938192-101501  
TDSFOT-26T84660

## FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAACTCCGGTAAGTACCTAGCCCACATGATT  
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATT CAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTCTTTTCC  
AGCCCTTGTCTCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATT CAGCATGTCACT  
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTTCTAACTTATTT CAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
TATGGATT CAGTGT CAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAA CAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT  
GTATTTGTGCGACCTACAGGTAGGCTAGTATTTATTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTTATTTTTTATTTATTTATTTTTTTGAGATAGGGTCT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTT CATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCCTA  
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCAGGCTGGAGTGCAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTTAGT  
AGAGACAGGGTTTCTCCATGTGCGT CAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT  
ACCATTTTTTT CAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
TGCTGATTTGTCTTATTTTTTTT CATACTTTCCCACTGGTGCTATTTTTTATTTCCAATGGATA  
TTTCTGTATTACTAGGGAGGCATTTACAGTCTCTAATGTTGATTAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTTATGTTATGTGGATTTTCAT  
TTCAATAAAAAAAACTCTTATCAAAAAA

09978192 "101501

## **FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFMSLSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

09978192 101501

# FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGGTCTCGCTCTGTCA  
 CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC  
 TCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGAATCCAGAGTGAATCCGTCCGAGGAGGAAAATGACTCCCCAG  
 TCGCTGCTGCAGACGACACTGTTCTGTGCTGAGTCTGCTCTTCCCTGGTCCAAGGTGCCCACGGCAGGGGCCACAGG  
 GAAGACTTTTCGCTTCTGCAGCCAGCGGAACAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG  
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTCCCTGCAGCCACCCCTGCTTCCCGA  
 TCCTTCCCTGACCCCAGGGGCTCTACCACTTCTGCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC  
 TATGGCAAGCGTGACTTCTTGTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG  
 GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC  
 GCCAGCTTACCTTCTCCTTCCACAGTCTCCCCACAGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC  
 AAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCCTCAAGGAGGCCCTCGGCTGCCCCC  
 GCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTTCATGGGGGACATGGTGTCTTTCGAG  
 GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCTCCAGGACCTGCACATCCACTCCCGG  
 CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC  
 CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAATTC  
 AGCTAAGTCTTGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACCTCACGGAGCCCGTG  
 GTGCTCACTTCCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTGGAAGACCCCCACA  
 TTGAGCAGCCCCGGGCATTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGC  
 AACCATTGACCTACTTTGCACTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC  
 CTCCTCTCTACGTGGGCTGTGTCTGTCTCTGCCCTGGCCTGCCTTGTCAACATTGCCGCCTACCTCTGCTCCAGG  
 GTGCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGGCCGTCTTC  
 ATCTTCCTGCACCTTCTCCTGCTCACCTGCCTTTTCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTG  
 GTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT  
 CTGGTGACGTGGTGGCCCTGGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG  
 GGCCTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTCACTACATCACCACCTGGGCCTCTTCAGC  
 CTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCACACCCAA  
 AAGTGGTCACATGTGTGACACTGCTGGGCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCC  
 TTTGCTTCTGGCACCTTCCAGCTTGTCTCTCTACCTTTTTCAGCATCATCACCTCCTTCCAAGGCTTCTCTCATC  
 TTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCCTCTGAAGAGCAACTCAGACAGCGCC  
 AGGCTCCCCATCAGCTCGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCCAGCCCACCTGCCCATGTGATGAAG  
 CAGAGATGCGGCCTCGTCGCACACTGCCTGTGGCCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACT  
 TTGGAAGCCCCAACGACCATGGAGAGATGGGCCGTGGCCATGGTGGACGGAATCCCGGCTGGGCTTTTGAATTG  
 GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCACAGGGACTCAGAAGTGCGCCGCCATGCTGCCCTAGGGTACTG  
 TCCCCACATCTGTCCCCAACCCAGCTGGAGGCCGTGGTCTCTCCTTACAACCCCTGGGCCAGCCCTCATTTGCTGGG  
 GGCCAGGCCCTTGATCTTGAGGGTCTGGCACATCCTTAATCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCA  
 GTTGCTCTGTCTCTCGTGGTCACTTGAAGGCACTCTGCATCCTCTGTCAATTTTAACCTCAGGTGGCACCCAGGG  
 CGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC  
 AGCTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCAGTCTCCTCCCTCATCTTCCCTGGGGTTC  
 TCCTCCTCTCCCAGGGCCTCCTTGTCTCCTTCCCTTACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGA  
 GTGGTTTTCCAGGAGCTGCCTGGTGTCTGCTGTAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCA  
 GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG  
 CTCACCCTGACCAAGCACACGCCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAATGTGGA  
 CCATGCCAGTCCCGTCTGGTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA  
 GAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT  
 TAATTCTGTCCAACAAACACACACGGGTAGATTGCTGGCCTGTGTAGGTGGTAGGGACACAGATGACCCGACCTG  
 GTCACCTCCTCCTGCCAACATTAGTCTGGTATGTGAGGCGTGCCTGAAGCAAGAACTCCTGGAGCTACAGGGACA  
 GGGAGCCATCATCTCCTGCCCTGGGAATCCTGGAAGACTTCTGCAGGAGTCAGCGTTCAATCTTGACCTTGAAGAT  
 GGAAGGATGTTCTTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTACATGTTTATTGTAGAGA  
 ATTTGGAAGTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAAAAA  
 AA



## FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRD FLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASF TFSFHSPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVD FSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLT EPPVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVV SALACLVTIAAYLCSRVPLPC  
RRKPRDYTIKVHNMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVF GTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGLIFIFIWYSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

### Important features:

#### Signal peptide:

amino acids 1-25

#### Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### Microbodies C-terminal targeting signal.

amino acids 691-693

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

#### N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### G-protein coupled receptors family 2 proteins

amino acids 475-504

09978192.101501

## FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCTGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTCTTCTGTTCAACATGG

0978192 101501  
TOSTOT" 26TB2660

# FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA  
 TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAAACTACCTT  
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC  
 TCGGGAGTCTGCTGCTTCCAAAGTGCCCGCGTGAGTGAGCTCTCACCCAGTGCAGCCAAATGAGCCTCTTCGGGC  
 TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
 AGTTTTTCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
 GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
 AGGAAAAATGTATGGATACAACCTTACGTTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
 ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
 GAAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
 TCTGCATCCACTACAACATTGTCTGTCACAAATTCACAGAAGCTGTGAGTCTTTCAGTGCTACCCCCCTTCAGCTT  
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG  
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGCTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTGGAA  
 GAAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT  
 CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG  
 GTGGGAACGTGTCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
 ACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
 ACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA  
 GAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCT  
 TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA  
 ACAGCTCTTTTGTAGAGGAGGCCTAAAGGACAGGAGAAAAGGCTTCAATCGTGGAAAGAAAAATTAAATGTTGTAT  
 TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC  
 GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCTTGTCTTAAC  
 TCTAAAGCTCCATGTCTGGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACAT  
 ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTAACTTGT  
 GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAAGAGAACTACA  
 TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG  
 TTTCAATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT  
 ATTTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACCTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCT  
 AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
 TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAAATTGGTAAGTTGCAAA  
 GACTTTTTGAAAAATAATTAAATATCATATCTTCCATTCTGTTATTGGAGATGAAAAATAAAAGCAACTTATGA  
 AAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
 AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAAGTAGGAACACATCCTATTTA  
 TTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTTATGTACA  
 GAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAAAATATTTTGTCTGT  
 AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAAATAAAGA  
 ATGTGGCTATTTTGGGGAGAAAAATTAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

105707-26787560

## **FIGURE 207**

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG

**Signal sequence:**

amino acids 1-14

09978192 101501  
105101 26184660

## FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGAAGA  
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCCTATCCTTTTAAACATAATCCTAATTTCC  
AAACTCCTTGGGGCTAGATGGTTTCTTAAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCTGGAGGTATCCCACGAACACCACGAACCTCACCCCTC  
ACCATTAACCACATACCAGACATCTCCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
TTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCCG  
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAACAACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA  
GATGCCTTCTTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCTACTGTT  
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
CTCAACCAATTACAAATTCCTGACCTAAGTGGAAATTGCCCTCGTTGTTATAATGCCCCATTTCTTGTGCGCCG  
TGTAATAATAATCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAGGTTTACGTCTA  
CACAGTAACTCTCTTACGATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC  
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCAGCCTCATCCAATTGGATCTG  
TCTTCAATTTTGAACCTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
AAAACTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
AATCTTGAAGTCTTGATCTTGGCACTAACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGA  
CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT  
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTGGAACAATTACATTATTTAGATATGATAAGTATGCA  
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCCCTGATTTTTCAGCATCTTCTTCTCAAATGCGCTG  
AATCTGTCAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTCACCTTTAGCAGAGCTGAGATATTTG  
GACTTCTCCAACAACCGCTTGATTTACTCCATTCAACAGCATTGGAAGAGCTTCACAACTGGAAGTCTGGAT  
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTTACCAAGAACCTAAAGGTT  
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAG  
AATCTGCTAAAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCTTCTGGAGTTTTTGATGGT  
ATGCCTCCAAATCTAAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT  
CTAAAGAACCTGGAACCTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAAGTGTCC  
AGAAGCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTCTACAAGATGCCTTC  
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTTC  
AACAACTGAAGATGTTGCTTTTGCATCATAATCGTTTTCTGTGCACCTGTGATGCTGTGTTGTTGTTGTTG  
GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTCTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT  
TTCTGTAAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATGTGTAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA  
CATTTTAATTTATGTCTCGAGGAAAGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA  
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTTAAGATAGCATTTTAC  
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG  
TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGAAGTGGCCAAACAAACCCGCAAGCTCAC  
CCATACTTCTGGCAGTGTCTAAAGAAGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCCTTCTTTGCAAAACAACTGCCTAGTTTACCAAGGAGAGGCCTGGC

09978192.101501

## **FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPOQLPPLSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR  
NPCYVSYSEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO  
TLDLSKNSIFFVKSSDFQHLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNKMLLLHHNRFLCTCAVWFVWVWNHTEVTIP  
YLATDVTCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPQGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 840-860

## FIGURE 210

GGGTACCATTTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAAACAGAAACATGGAACATGTTCCCTTC  
AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCTGTGAGTTATGCGCCGAGAAAAATTTTCTA  
GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCCGACTACAGGAAG  
TTCCCCAAACGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAAT  
CATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC  
CCGGTATACAAATCAAATGGCTTGAATATCACAGACGGGGCATTCTCAACCTAAAAAACCTAAGGGAGTTACTGC  
TTGAAGACAACCAAGTTACCCCAAATACCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA  
ATATATACAACATAACTAAAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACGTCT  
ATTTTAACAAAGTTTTCGAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT  
CCTATCTTTCAATTTCTTTTACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA  
CCCAGATCAAAATACATTTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAACT  
GTCCGAGGTGCTTCAATGCCCCATTTCATGCGTGCCTTGTGATGGTGGTGCCTCAATTAATATAGATCGTTTGTG  
CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT  
TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
TTTTAACGATGCTGCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATA  
TTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC  
TCAGAGAAGATGATTTCCAGCCCTGATGCAGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA  
AGCAAATCGATTTCAAACCTTTCCAAATTTCTCCAATCTGGAATTTATTTACTTGTGAGAAACAGAAATATCAC  
CGTTGGTAAAAGATACCCGGCAGAGTTATGCAAATAGTTCTCTTTTCAACGTATATCCGGAACGACGCTCAA  
CAGATTTTGGTTTGGACCCACATTCGAACCTTTTATCATTTACCCGTCCTTTAATAAAGCCACAATGTGCTGCTT  
ATGGAAGCCCTTAGATTTAAGCCTCAACAGTATTTTCTTCAATTGGGCCAAACCAATTTGAAATCTTCTGACA  
TTGCTGTTTAAATCTGCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAACCTGAATTTTCCAGCATTCTCATG  
TCAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTTGTCGGACTTGG  
AAGTTCTAGATCTCAGCTATAATTCACACTATTTGAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCAA  
ATTTCACAAATCTAAAGTTTAACTTTGAGCCACAACAACATTTTATACTTTAACAGATAAGTATAACCTGGAAA  
GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA  
TCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATG  
AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACCTACATAAATGATAATATGTTAAAGTTTAACTGGA  
CATTACTCCAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGATAGCC  
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCTCTGGCTTTC  
TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG  
AACTAAGACCACCACCAAAATATCTATGTTGGAATACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG  
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTTCCAGACTGGTAGATGTCAATTTGTGCCAGTCTG  
GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACCACTTGTGTTTCCAGATGTCACTGAGTGAATTTAT  
TTTTCTTCCAGTTCTTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTGTGTTTAACTGGGATGTTT  
GGTTTATATATAATGTGTGTTTAGCTAAGGTAAGGCTACAGGTCTCTTTCCACATCCCAAACCTTTCTATGATG  
CTTACATTTCTTATGACACCAAGATGCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG  
AGAGCCGAGACAAAAAGCTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC  
TCATGCAGAGCATCAACCAAGCAAGAAACAGTATTTGTTTAAACCAAAAAATATGCAAAAAGCTGGAACCTTTA  
AAACAGCTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAATGATGATGATTATATTTTCTGCTGGAGC  
CAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA  
ACCCGAAGGCAGAAGGCTTGTGTTTGGCAAACCTCTGAGAAATGTGGTCTTGACTGAAATGATTACGGGTATAACA  
ATATGTATGTGATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTGCGGCCATAATAAGATGCAAG  
GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATATCCCAAACTTAGTGGTTTAAACAACACA  
TTTGCTGGCCACAGTTTTTGGGGTCCAGGATCCAGGCCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG  
AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGGTCACTCATGTGGTGTGTTTCTGGATTCA  
ATTCTCTGGGCTATTGGCCAAAGGCTATACCTCATGTAAGCCATGCGAGCCTCTCCCAAGGCGAGCTTGTCTT  
ATCAGAGCTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAGTGAT  
ATCTCATCACTTTGGCCATATTCTATTTGTTAGAGTAACACAGGTCCACCAGCTCCATGGGAGTGACCACC  
TCAGTCCAGGGAAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCACTGGTCACTAATTTTCCCT  
TGACTGCTGTCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC  
ATCTTAGCAGTTGACCTAACACATCTTCTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATA  
TTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGGTTTATATGCTGTGGTTGCGTTGCGTTTAT  
TTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAACTGAGATGG  
ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATA  
TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

## FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQND SVIAECSNRRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNL TQLRYLNLSSTSLRKINAAWFKNM  
PHLKVLDFEYNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELEV  
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNNDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHL DLS  
SNLLKTINKSALETKT TTKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQT FYDAYISYDTKDASVTDWVINE LRYHLEESRDKNVLLCLEERDWD PGLAIID  
NLMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVII FILLPEVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLEFWQTLRNVVLTENDSRYNMYVDSIKQY

### Signal sequence:

amino acids 1-26

### Transmembrane domain:

amino acids 826-848



## FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTCCTG  
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTTGACTGCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTGA  
AAAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

## FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSadGTLCVpKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978192.101501  
"05101" 2618/660

## FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGGCCGGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCG  
TGCAGCGTGTGTACCAGCCCTTCTCACCACTGCGACGGGCACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCTTCTTCTGGAGGAGCAGCTGGGGTCTTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCTCCTCTTCTCCTCCCCCTTCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACATAAAAAATGAAACGTG

09978192.101501

## FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978192.101501  
TOSTOT" 26T8/660

## **FIGURE 216**

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT  
GGGGTCTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTG

09978192.101501

## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSL SADGTLCV PKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

09978192-101501  
TOSTOT-26187660

## FIGURE 218

GGTTGCCACAGCTGGTTTATAGGGCCCCGACCACTGGGGCCCCCTTGTCTAGGAGGAGACAGCCTCCCCGGCCCCGGGGAG  
GACAAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACCGTCCGTTTCTCTGCCGTGAGCTGCCGGCCG  
AGTTGGGTCTCCGTGTTTTCAGGCCGGCTCCCCCTTCTCTGGTCTCCCTTCTCCCGCTGGGCCCCGTTTATCGGGAGG  
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT  
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGTAAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATCA  
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGGAACACCTTTTGCTGTG  
ATGGCCCGCTCATGATGGCCCCGGCAAAAGGGCATTTCCTACCTGACCCCTTTCTCTCATCTGGGGACATGTACAC  
TCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTGTTGAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT  
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCCTGGAGTGATTCTCTCGGGCGCTACCAGATG  
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGGACACCGCCTCGTA  
TCAAGAATTTCCAGATAAAACAACCAGATTGTGAAACTGAAATACCTGTTACACATGCAAGATCTTCCGGCCTCCCC  
GGGCTCCCATTGCAGCATCTGTGACAACCTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG  
TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCT  
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAAGCTG  
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTGCTGGGACTGACTGGATTTCATACTTTCTCTGCTGG  
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTG  
TTTTGCCACTGGAGGAAAGTGGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC  
CAGCCCCCAGAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG  
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTGTT  
TAATTAGGGCTATGAGAGATTTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT  
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTCCTTGCTGCAAGCTTTTTTAAATTTCTGAACT  
CAAGGCAGTGGCAGAAGATGTGAGTCACCTCTGATAACTGGAATAATGGGTCTCTTGGGCCCTGGCACTGGTCT  
CCATGGCCTCAGCCACAGGGTCCCCCTTGGACCCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC  
TGGTCTCATTTCTGGGGCTAAAAGTTTTTGGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG  
TGGGTCCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT  
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTGACTCCTGCTCCCATTAGGAG  
CAGGAATGGCAGTAATAAAAGTCTGCACCTTTGGTCATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC  
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAAGTTCTTCCATTAAGCCT  
CGGCTGAGTGAGGGAAAGCCCAGCACTGCTGCCCTCTCGGGTAACCTACCCCTAAGGCCTCGGCCACCTCTGGCT  
ATGGTAACCACTGGGGGCTTCTCCTCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT  
CACCTTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT  
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT  
GCGGTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

09978192 "401501  
TOSTOF" 267866

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL  
FILSLSLLTIYVFAFNIVYVALKSLKIGFLETCLKETPGTVLEVLCFFTLWSVVGLTGFTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPPQEAAEAEK

### **Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

105701 26782660



## FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCCTTTTGGCTTTGGACTCTCNCTTTCT  
CCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

09978192 101501  
"FOSTOT" 26TB4660

## FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTGTAGAGATTTCT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAACACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACCTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAAATTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGAACCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

## FIGURE 222

MKTIQPKMHNSISWAIIFTGLAALCLFQGVVRSRGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECsasNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTLOCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNVTCVASNKLIGHTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

**Signal peptide:**

amino acids 1-28

09978152-101501  
TOSTOT-2518/660

## FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

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## FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCCGACTCCACCATGAACCTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA  
GAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGCTGGATTGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACCAAACAGGCCATACTGAAGCACCTGCTTGAAAAACACACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCCATCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAACTGCTGGAGACCTCTATGGCACTAAGAAG  
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGAACGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTATGGCTGACCAGCTCCGCAAG  
CCTCCCAGCCGAGACCACTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACTTCGGTGGCATC  
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACAGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG  
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACCACTCTTCTTCTGTTGGGATTTGCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG  
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTTGCGG  
CACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGTCTTGGGTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCACAGGTGACATGAGTACAGACCCCTCCTCAATCACCACATTG  
TGCCCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT  
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

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## **FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQ NQA  
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQ DN  
FMEVLKAVAGTYRATPFFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVL TAY  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQ LANITVPODQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLLETLYGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFQAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

**Type II Transmembrane domain:**

amino acids 32-57

1. General Information	
Item	Value
1.1. Name of the Project	Project Name
1.2. Date of Submission	Submission Date
1.3. Version	Version Number
1.4. Author	Author Name
1.5. Contact Information	Contact Details
1.6. Summary	Project Summary
1.7. Objectives	Project Objectives
1.8. Scope	Project Scope
1.9. Deliverables	Project Deliverables
1.10. Risks	Project Risks
1.11. Budget	Project Budget
1.12. Timeline	Project Timeline
1.13. Stakeholders	Project Stakeholders
1.14. Conclusion	Project Conclusion
1.15. Appendix	Project Appendix
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CCGCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCGCTCCCGGCCCTCCTCCCTCCCTCCTCCC  
CAGCTGTCCCCTTCGCGTTCATGCCGAGCCTCCCGGCCCGCCGGGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCT  
CGGCTCCCGGCCCGGCCCGCGCGCCCGCCAGAGCCCCCGTGTGCCCATCCGTTCTGAGAAGGAGCCGCTGCC  
CGTTCCGGGGAGCGGCAGGTAGGTAGGCGCGCCCGGGGAGGCGCGGGCGGGGAGTCCGGCTCGGGGCGAGTCAGCGC  
CAGCCCGGAGGGGGCGCGGGGCGCAGGTGGCTCGGCGCGGCGCGGCCCGGAGGGTGGGCGGGGGCAGAAGGC  
GCGGTGCCCTGGGACCCCGGACCCCGCGGGCAGCCCCCGGGCGGACACCGCGCGAGCTGGGCAGCGGCTCCAGC  
CAAGCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCCCTTGACGAGACGTGGCACCCGGACCTAGG  
GGAGCCATTCCGGGGTGATGCGCTGCGTGCTGTGCGCTTGCAGAGGCGCAGTGGGGTGCGCCGTACCAGGGGCCCTGG  
CAGGGTCCAGCTGCAAGAACATCAAACCAGAGTGGCCAAACCCCGGCTGTGGGCAGCCGCGCCAGCTGCCGGGACA  
CTGTGCCAGACCTGCCCCCAGGACTTCGTGGCGCTGTGTACAGGGCCGAGGTGCGAGCGGTGGGACAGAGCCCC  
AGTCTCGTGTCTGCGTCTAGCCTTCGCTCTCTATCTCCTACAGCGGCTGGACCGCCCTACCAGGATCCGCTT  
CTCAGACTCCAATGGCAGTGTCTGTGTTGAGCACCTGACGCCCCACCAAGATGGCTGGTCTGTGGGGTGTG  
GCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTACTCA  
CCCTTCAGGGGAGGTCTGGGGGCCCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGAC  
TCTAGAAGGCCCCCCACCAGCAGGGCGTAGGGGGCATCACCTTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA  
TTTTTTGCTGCTCTTCGAGGCCCTTGCAAGACTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCA  
GCTACTGCGAGAACTTCAGGGCCAATGTTTCAGCCAGGAACAGGCTTTGTGTAGGTGCTGCCCAACCTGACAGT  
CCAGGAGATGGACTGGCTGGTGTCTGGGGGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCAT  
CAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGTCTTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC  
AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCTCCAGGTGCAATT  
GGTAGGACAAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTCAGCGGAGGGATCAGCCCACTGTCTT  
GTGCCACATGGCTGGCCTATCCTCCCCGCCCCAGGCCGTGGGTATCTGCCCTGGGCTGGGGTGGCCGAGGGGC  
TCATATGCTGTGCGAGAATGAGCTCTTCCTGAACGTGGGCACCAAGACTTCCAGACGGAGAGCTTCGGGGGCA  
ACGTGGCTGCCCTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTACC  
CCCTGTGAAGAGCCAAGCAGCAGGGGCACGCCTGGCTTTCTTTGGATACCCACTGTCACTTGCATATGAAGTGCT  
GCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCACCTCCTTTGGGCTCCTTGAACGCGCAGGGCC  
TCGGCGGCTGTCTGAAGGGATTCTATGGCTCAGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACTGCTGCG  
GCACCTGCGCAAAAGGCATGGCTTCCCTGTATGATCACCACAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT  
CTCCTCCAGGTGCACATAGCCAACCAATGTGTAGGTTGGCGGACTGCGCTTGAGGCGCGGGGCGAGGGGCT  
GCGGGCGCTGGGGCTCCGGATACAGCCTCTGCTGCGCGCCCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC  
CAAACCTGGTGGTCTTGGGCGGCCCCGAGACCCCAACACATGCTTCTTCGAGGGGCAGCAGCGCCCCCACGGGGC  
TCGCTGGGCGCCCCAACTACGACCCGCTCTGCTCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGT  
GGTGTGCCCAACCGCCAGCTGCCCAACCCGGTGACGGCTCCCGACCAAGTGCTGCCCTGTTTGCCCTGGCTGCTA  
TTTTGATGGTGAACCGGAGCTGGCGGGCAGCGGTTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGCTTAATTA  
GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACCTGTGAGAAGGTGCAGTGTCCCCGGTGGC  
CTGTGCCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGGTGAGGCCCCACCCCACTGGG  
GGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGTGCTGGGCAGTGGTTCCAGAGAGTCAGAGCTGGCA  
CCCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT  
GTGAGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCAGGGAGGTCCTGAAGAAGCTGAAGGTCA  
CTGTGTCCCAGTGCCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACCAGGAGGTTGCCCTCACTGTGAG  
GGATGACTGTTCACTGCCACTGTCTTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTCCCGCTGCACGGCCACC  
GGCGGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCCTGTGGGACTCCTGATCAG  
GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCCTCACAAGTGCCATTCCAATCCACCCCTCACAGCA  
ACCTGGTGGAAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTCTGAAGCTCAGAGAAATTAAGCAACCGT  
ATGAAGTCAACCCAGCTGTGTGCACCTGACCTGTTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGATGCTT  
TGCCCTGCCCTCTATGCCCTCTCTGTGCCCTTCCACTCCCTCCTCCCTCCAACATTCCTCCCTCTGTCTCC  
AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC  
AAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCACTTCTCCTGTGGGAAG  
CCAGTGCCCTTTGCTCCTCTGTCTTGCCTCTACTCCCAACCCCACTACCTCTGGGAACCAAGCTCCACAAGGGG  
GAGAGGCAGCTGGGCGAGACCGAGTATCAGCCCACTCCAAGTCTCGCCCTGCCACCCCTCGGCCTCTGTCTGGAA  
GCCCCACCCCTTTCTCTCTGATCATAGTGCACCTGGCTTGTGGGATTTTTTAATTTATCTTCACTCAGCACCAAG  
GGCCCCGACACTCCACTCCTGCTGCCCTTGAGCTGAGCAGAGTCATTATTTGAGAGATTTTTGTATTTATTA  
AATTTCTTTTTTCACTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCTGGTGGAGAAGGG  
GCNAGAGTAGGAGGTGAGAGAGAGGAGCTTGACACTTGGGGAGCTGAAAGAGACCTGGAGAGGCAGAGGATAG  
CGTGGCCTTTGGCTGGCAATNCCTGGGTTCCGCAAGAGGGGCTGGGGATGGTTCTTGAGATGGTCTAGAGACTCAAG  
AATTTAGGGGAAGTAGAAGCAGGATTTTGACTCAAGTCTTAGTCTCCACATCGCTGGCCTGTTTGTGACTTCAATG  
TTTTGAAGTTGCTCCAGAGAGAGAATCAAAGGTGTCACCAGCCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTCT  
TTCCCTCCCCCTCCCCCTCCCCCTCCCCCTCCCCCTC

## FIGURE 227

GGCCGAGCGGGGGTGTCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGCCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC  
TCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA  
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCT  
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCCTTCCCTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCTG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

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## **FIGURE 228**

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCC  
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTG CATATGTGTAGCGGGTACTGGTTCCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

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## FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
 GGAGGGGAGGCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG  
 GGGGAAGAAAGAAAGAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
 TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
 CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG  
 CTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG  
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT  
 TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTTCACTCAACATACACCCAGAACA  
 ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA  
 TTTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT  
 TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGGGAAATGCTGTGTGCTATT  
 CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTCAGGAAATTAAAT  
 CTGGCACCGTGACCCCCGACGCGAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCCCT  
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT  
 TCAAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCCT  
 CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTCTCCTGCTGGTACCT  
 TGTGTTGACACTGTCCTCTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA  
 TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
 GGTACAGTTTGTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC  
 TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTTGATTAGCTACATTA  
 CCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG  
 AGGATATTAATTGTGATTTTATGTTTGTAACTTACAACCTTTTCAAAGCATTTCAGTCATGGT  
 CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATTGCAGTGAATATGTGATTCTTTAA  
 GGCTGCAATACAAGCATTTCAGTTCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG  
 CATTTTTTTCTTTTTTTGATAAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA  
 TAACACATATCTAGATTTTTCTGCTTGCATGATATTTCAGGTTTCAGGAATGAGCCTTGTAAT  
 ATAAGTGGCTGTGCAGCTCTGCTTCTCTTTCTGTAAGTTTCAGCATGGGTGTGCCTTCATAC  
 AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTTGCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT  
 AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTT  
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA  
 GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAA  
 TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA  
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
 AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA  
 CAAGGAATAATTTCTGATCCAGGATCGTCCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG  
 AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTGACCTGCCA  
 AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA  
 AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSII FAGGDKWSVDPRVSI STL NKR DYS LQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILT VTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLK NAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

09976192.101501

## FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA  
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG  
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACTTCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTCACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAAGGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCAAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT  
GGCCCAAAGGGGAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCTCCTGGAGCCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC  
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCTTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC  
GTCAGGATTGTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGACCCCGAAACCCTTTCA  
CTTCTCTGCTCCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATGA

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## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPF EINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD  
GATGPSGPQGPVGKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE  
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGFGRPGPPGLAGFPGAKGDQGPGLQGVPG  
PPGAVGHGPAKGEPPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGGLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSEGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLW  
SCTKNSWGHHDCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

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105101 26182660

## **FIGURE 233**

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG  
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTC  
CCACAAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAA

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TOSTOT"26T82660

## **FIGURE 234**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1 .

MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG  
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNO

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-76

**Tyrosine kinase phosphorylation site.**

amino acids 63-71

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105101.26182660

# FIGURE 235

CCCACGCGTCCGCGGACGCGTGCGGCTGGACCCCAGGTCTGGAGCGAATTCAGCCTGCAGGG  
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC  
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCAGGAGGCCGGCTCTGCTCGCGCCGAGATG  
 TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG  
 CGCTGGGGCGCTGGTGCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA  
 TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTTGAT  
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC  
 AGGAACAGAACAAAACCTTTAGCTTGCAAAGCAAATTCATCCAGTGGAAGAATTTGGCC  
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTACCCAAATAAGACTCATCCC  
 AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC  
 ACCTCCTCCAGGATATGAAAATGTTTTCGGATATTGTACCACCTTTCAGTGCTTCTCTCCTC  
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA  
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT  
 TTTAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT  
 CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCCT  
 GGAGGTGGTGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCTCTCACACC  
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAA  
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC  
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG  
 CTTTACTGGAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA  
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT  
 CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT  
 TGTTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA  
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC  
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG  
 ACTAAAAAAGTCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAAGCAAATTTGGGATCTGG  
 AAATGATTTTGGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA  
 AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT  
 GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG  
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTCGAGATTATG  
 CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
 ATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT  
 TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA  
 TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTTATTGATCCATTAGGGTTACCAGAC  
 AGGCCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC  
 ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCTTCCAAGGCCCT  
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT  
 TTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA  
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGT  
 TGAATATTATATATAA



## **FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFL  
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH  
PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF  
KLERDMKINCSGKIVIRYGVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL  
PGGGVQRCNINLNLNGAGDPLTPGYPANAYRRGIAEAVGLPSIPVHPIGYYDAQKLLKMG  
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDYV  
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW  
AEENSRLLOERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYES  
WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET  
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ  
EMKTYSVSFDLFSVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP  
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE  
TLSEVA

### **Signal sequence:**

amino acids 1-40

### **N-glycosylation sites.**

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

### **Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

### **N-myristoylation sites.**

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713